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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 13.4088 Seconds

(without alignments)
189.646 Million cell updates/sec

Title: US-09-720-469A-1

Perfect score: 49

Sequence: 1 KFRHVIKDF 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	3	AAV69921 Human cyc
2	49	100.0	9	4	AAAB46930 Human cyc
3	49	100.0	9	4	AAAG68088 Antitumou
4	49	100.0	9	5	ABG79075 Human Cyp
5	49	100.0	9	6	ABR84373 Human Cyp
6	49	100.0	9	7	ADCI7701 Cyclophil
7	46	93.9	9	3	AAV69962 Human cyc
8	46	93.9	9	4	AAAB46946 Human cyc
9	36	73.5	9	4	AAV69960 Human cyc
10	32	65.3	11	3	AAV69924 Human cyc
11	32	65.3	11	3	AAV69924 Human cyc
12	29	59.2	11	2	AAAR48203 Human pho
13	29	59.2	12	1	AAAP93365 Amino aci
14	29	59.2	13	2	AAAR62271 Phospholi
15	29	59.2	14	2	AAWS8475 Human TYP
16	29	59.2	14	7	ADD84475 121P1f m
17	27	55.1	10	2	AAAR6521 Hepaticis
18	27	55.1	11	4	AAAB82292 Phosphory
19	27	55.1	12	2	AAW92359 CYP2B1 im
20	27	55.1	14	4	AAW92359 CYP2B1 im
21	26	53.1	9	5	ABG94771 Replikin
22	26	53.1	9	5	ABG94772 Replikin
23	26	53.1	9	6	ABU57321 Replikin
24	26	53.1	9	6	ABU57322 Replikin
25	26	53.1	9	7	ADD82912 121P1f m

26	26	53.1	9	7	ADD83072 121P1f m
27	26	53.1	9	7	ADD84184 121P1f m
28	26	53.1	9	7	ADD84174 121P1f m
29	26	53.1	9	7	ADD83046 121P1f m
30	26	53.1	9	7	ADD83134 121P1f m
31	26	53.1	9	7	ADD83215 121P1f m
32	26	53.1	9	7	ADD84124 121P1f m
33	26	53.1	9	7	ADD84150 121P1f m
34	26	53.1	9	7	ADD83010 121P1f m
35	26	53.1	9	7	ADD84169 121P1f m
36	26	53.1	9	7	ADD84188 121P1f m
37	26	53.1	9	7	ADD82989 121P1f m
38	26	53.1	9	7	ADD83208 121P1f m
39	26	53.1	9	7	ADD82979 121P1f m
40	26	53.1	9	7	ADD83263 121P1f m
41	26	53.1	9	7	ADD82850 121P1f m
42	26	53.1	9	7	ADD82866 121P1f m
43	26	53.1	9	7	ADD83127 121P1f m
44	26	53.1	9	7	ADD83203 121P1f m
45	26	53.1	9	7	ADD84128 121P1f m

ALIGNMENTS

RESULT 1

AAV69921 standard; peptide, 9 AA.

11-APR-2000 (first entry)

Human cyclophilin B peptide fragment #1.

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

HIV antigen; diagnosis; tumour; therapy.

Homo sapiens.

24-JUN-1999; 99WO-JP003360.

25-JUN-1998; 98JP-00178449.

(SUMU) SUMITOMO PHARM CO LTD.

(ITOH) ITOH K.

Itoh K, Gomi S;

WPI, 2000-116932/10.

Tumour antigen peptides derived from cyclophilin B for treatment and

diagnosis of tumors.

Claim 4; Page 49; 64pp; Japanese.

This sequence represents a cyclophilin B peptide of the invention. The

peptides are tumour antigen peptides derived from cyclophilin B, that

recognize cytotoxic T-cells (CTL) which bind to the HIV antigen. The

peptides are used for the treatment and diagnosis of tumours

Sequence 9 AA;

Query Match 100.0%; Score 49; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KFRHVIKDF 9

Db 1 KFRVIXDF 9

DE Antitumour peptide cyclophilin B 94-92.

XX Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;

XX tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;

KW cyclophilin B gene; HLA-A2402.

OS Homo sapiens.

XX JP2001245675-A.

PN 11-SEP-2001.

XX

PD 25-DEC-2000; 2000JP-00393047.

XX

PF 28-DEC-1999; 99JP-00374322.

XX

PR (ITOY/) ITO Y.

XX

PA WPI; 2001-610076/70.

XX

DR New peptides for recognizing cancer cells with tumor specific cytotoxic T

XX lymphocytes and for treating cancer.

PT Claim 8; Page 2; 14pp; Japanese.

XX

PS The present invention describes peptides recognising cancer cells with

XX tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising

CC cancer cells with tumour specific CTLs are selected from: (1) peptides of

CC sequences (AAG68066 to AAG68069); (2) peptides containing the above

CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with

CC the above mentioned sequences; and (4) peptides with one or more deleted,

CC substituted, added or inserted amino acid(s) of the above mentioned

CC sequences, particularly those having recognising property due to HLA-

CC A2402 binding CTL, especially having at least 5 amino acids, used for

CC medicine, particularly anticancer agents, derived from antitumour

CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B

CC genes. The antitumour peptides have cytostatic activities. The peptides

CC are used for the treatment of cancer. The peptides cause activation of

CC CTL in cancer patients. The present sequence represents a peptide from

CC the present invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFRVIXDF 9

Db 1 KFRVIXDF 9

DE Human Cyp-B class I HLA widely expressed antigen peptide #1.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;

KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;

KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;

KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;

KW ovarian cancer; pancreatic cancer; eploipe; vaccine; dendritic cell;

KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;

XX cytostatic; human.

XX Homo sapiens.

OS

XX

RESULT 3

AAAG68088

ID AAG68088 standard; peptide; 9 AA.

XX

AC AAG68088;

XX

DT 17-DEC-2001 (first entry)

XX

DE Antitumour peptide cyclophilin B 94-92.

XX

XX Antitumour; cancer; cancer cell recognition; antigenic; CTL; lck; src;

KW tumour specific cytotoxic T lymphocyte; anticancer; SART-1; SART-3;

KW cyclophilin B gene; HLA-A2402.

OS Homo sapiens.

XX JP2001245675-A.

PN 11-SEP-2001.

XX

PD 25-DEC-2000; 2000JP-00393047.

XX

PF 28-DEC-1999; 99JP-00374322.

XX

PR (ITOY/) ITO Y.

XX

PA WPI; 2001-610076/70.

XX

DR New peptides for recognizing cancer cells with tumor specific cytotoxic T

XX lymphocytes and for treating cancer.

PT Claim 8; Page 2; 14pp; Japanese.

XX

PS The present invention describes peptides recognising cancer cells with

XX tumour specific cytotoxic T lymphocytes (CTL). The peptides recognising

CC cancer cells with tumour specific CTLs are selected from: (1) peptides of

CC sequences (AAG68066 to AAG68069); (2) peptides containing the above

CC mentioned sequences; (3) peptides having 70 % or more of homogeneity with

CC the above mentioned sequences; and (4) peptides with one or more deleted,

CC substituted, added or inserted amino acid(s) of the above mentioned

CC sequences, particularly those having recognising property due to HLA-

CC A2402 binding CTL, especially having at least 5 amino acids, used for

CC medicine, particularly anticancer agents, derived from antitumour

CC antigenic peptides of lck, src family, SART-1, SART-3 or cyclophilin B

CC genes. The antitumour peptides have cytostatic activities. The peptides

CC are used for the treatment of cancer. The peptides cause activation of

CC CTL in cancer patients. The present sequence represents a peptide from

CC the present invention

XX

SQ Sequence 9 AA;

Query Match 100.0%; Score 49; DB 4; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KFRVIXDF 9

Db 1 KFRVIXDF 9

DE Human Cyp-B class I HLA widely expressed antigen peptide #1.

XX Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen;

KW lymphoma; sarcoma; lung cancer; non-Hodgkin's lymphoma; leukaemia;

KW Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;

KW kidney cancer; adenocarcinoma; breast cancer; prostate cancer;

KW ovarian cancer; pancreatic cancer; eploipe; vaccine; dendritic cell;

KW tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;

XX cytostatic; human.

XX Homo sapiens.

OS

XX

RESULT 4

ABG79075

ID ABG79075 standard; peptide; 9 AA.

XX

AC ABG79075;

XX

DT 15-NOV-2002 (first entry)

XX

PN WO200264057-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 15-FEB-2002; 2002WO-US005212.
 XX
 PR 15-FEB-2001; 2001US-0268687P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Wang R;
 XX
 DR WPI; 2002-627577/67.
 XX
 PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 XX
 PS Disclosure; Page 17; 61pp; English.
 XX
 CC The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigen
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 49; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFHRYIKDF 9
 DB 1 KFHRYIKDF 9
 RESULT 5
 ABR84373
 ID ABR84373 standard; peptide; 9 AA.
 XX
 AC ABR84373;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human CypB HLA-A24 epitope; SEQ ID NO:23.
 XX
 KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
 KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
 KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
 KW human; human leukocyte antigen; HLA-A24 epitope.
 XX
 OS Homo sapiens.
 OS
 PN JP2002365286-A.

XX
 PD 18-DEC-2002.
 XX
 PF 18-SEP-2001; 2001JP-00283413.
 XX
 PR 13-NOV-2000; 2000JP-00345094.
 XX
 PA (ITOY/) ITO Y.
 XX
 DR WPI; 2003-508315/48.
 XX
 PT A detection method of antigen specific T-cells, comprises the use of
 PT plural antigenic peptides, useful in semi-quantitative determination of
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.
 XX
 PS Example 8; Page 10; 18pp; Japanese.
 XX
 CC The invention relates to a method for the detection of antigen specific T
 CC cells in a blood sample involving the use of a plurality of antigenic
 CC peptides. The method comprises sampling of peripheral blood monocytes;
 CC stimulation of the collected peripheral blood monocytes with antigens
 CC without direct use of antigen presenting cells; and detection of T-cells
 CC specific to the antigen in the stimulated monocytes. The method is
 CC particularly used for the detection of cancer as it can be used in semi-
 CC quantitative determination of cancer specific T-cells. It can also be
 CC used for cancer vaccine therapy for patients with cervical or prostate
 CC cancer. The method can additionally be used to monitor of cellular
 CC immunity and cancer immune therapy by detection of specific T-cell
 CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
 CC leukocyte antigen) peptides of human origin used in an example from the
 CC invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 48; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KFHRYIKDF 9
 DB 1 KFHRYIKDF 9
 RESULT 6
 ADC17701
 ID ADC17701 standard; peptide; 9 AA.
 XX
 AC ADC17701;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Cyclophilin B protein amino acids 84-92.
 XX
 KW Cytostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;
 KW allergy; epitope; cancer; immunoglobulin B antibody; desensitization;
 KW cyclophilin B.
 XX
 OS Synthetic.
 OS
 PN MO2003020306-A1.
 XX
 PD 13-MAR-2003.
 XX
 DE 28-AUG-2002; 2002WO-JP008641.
 XX
 PF 29-AUG-2001; 2001JP-00260046.
 XX
 PR (ITOH/) ITOH K.
 XX
 PA Itoh K, Yamada A;
 XX
 PI Itoh K, Yamada A;
 XX
 DR WPI; 2003-300831/29.

PT Deesensitizers or allergic reaction suppressors containing peptides originating from the same antigenic substances as reaction-inducing PT substances, useful for preventing or treating type I allergic diseases and in cancer vaccines.

PS Claim 8; SEQ ID NO 1; 49pp; Japanese.

CC The invention relates to allergic reaction suppressors, comprising a
CC peptide which originates from the same antigenic substance as the
CC antigenic substance inducing the (peptide-originated) allergic reaction,
CC and containing an epitope different from the epitope participating in the
CC induction of the allergic reaction and yet does not induce the allergic
CC reaction. The desensitizers or allergic reaction suppressors are useful
CC for treating and preventing type I allergic diseases and in cancer
CC vaccines for preventing or treating cancer. The allergic reaction
CC suppressors are also useful for suppressing an allergic reaction or
CC reducing immunoglobulin B antibody production, and for desensitization to
CC antigens. This sequence represents a peptide used in the invention and
CC corresponds to amino acids 84-92 of the cyclophilin B protein.

SQ Sequence 9 AA;

```

Query Match      .100.0%; Score 49; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0

```

QY	1	KEHVRV	KDF	9
Db	1	KEHVRV	KDF	9

RESULT 7
AAY69962

AC AAY69962;

DT 11-APR-2000 (first entry)

DE Human cyclophilin B peptide fragment #42.

KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

KW HLA antigen; diagnosis; tumour; therapy

OS Homo sapiens.

PN WO9967288-A1.

PD 29-DEC-1999.
 YY

PF 24-JUN-1999; 99WO-JP003360.
 YY

25-JUN-1998; 980P-001/8449.
PR
XX

PA (SUMC) SUMMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K
PA (ITOH/) ITOH K

XX
PI
Itoh K.
Gomi S

WPI: 2000-116932/10.

PT Tumor antigen peptides derived from cyclophilin B for treatment and
PT diagnosis of tumors.

PS Claim 10; Page 60; 64pp; Japanese.

CC This sequence represents a cyclophilin B peptide of the invention. The
CC peptides are tumour antigen peptides derived from cyclophilin B, that
CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC peptides are used for the treatment and diagnosis of tumours

SQ Sequence 9 AA;

Query Match	93.9%	Score 46;	DB 3;	Length 9;
Best Local Similarity	88.9%	Pred. No. 1.4e+06;		
Matches	8;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy	1	K E H R V I K D F	5
		:	
Db	1	K Y H R V I K D F	5

RESULT 8	
AAB46946	
ID	AAB46946 standard; peptide; 9 AA

AC AAB46946;

DT 04-MAY-2001 (first entry)

DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 32.

KM Tumor antigenic peptide; interferon; IFN; antigen-specific T cell
KM vincide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
KM viral infectious disease; cyclophilin B; human.

OS Homo sapiens.

PN EP1074267-A1.
yy

PD 07-FEB-20
yy

PF 24-JUL-2000; 2000EP-00306263
XX

PR	22-JUL-1999;	99JP-00207687
XX		

FA (SUMO) SUMITOMO PHARM CO LTD.
XX

XX
Pl Takasu H., Golon M., Iamacka I.,

DR WPI; 2001-193144/20.

PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
PT the manufacture of an agent for the induction of antigen-specific T
PT cells.

PS. Disclosure; Page 19; 25pp; English.

CC This invention describes the novel use of interferons (IFNs) or DNAs
CC capable of expressing the interferons and/or antigenic proteins (AP),
CC antigenic peptides derived from the proteins or DNAs capable of
CC expressing the antigenic proteins or peptides, in the manufacture of an
CC agent for induction of antigen-specific T cells. The products of the
CC invention have virucide and cyostatic activity and can be used for gene
CC therapy or as inducers of antigen-specific T cells. The action of
CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
CC T cell (CTL) by administering an antigenic peptide in an incomplete
CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
CC DNA encoding IFNs) are useful in the manufacture of a medicament for
CC inducing antigen-specific T cells in an individual who has been
CC administered with AP (or DNA encoding AP) or vice versa. The medicament
CC is useful for the treatment or prophylaxis of a tumor or a viral
CC infectious disease

SQ Sequence 9 AA;

Query Match	93.9%	Score 46;	DB 4;	Length 9;
Best Local Similarity	88.9%	Pred. No. 1.4e+06;		
Matches	8;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

QY	1	KEHRVIKDF	9
		:	
Db	1	KYHRVIKDF	9

RESULT 9

AA69960	standard; peptide; 9 AA.
AA69960;	
11-APR-2000	(first entry)
Human cyclophilin B peptide fragment #40.	
Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.	
Homo sapiens.	
Key	Location/Qualifiers
Misc-difference 2	/label= Phe, Tyr, Met, Trp
Misc-difference 9	/label= Phe, Leu, Ile, Trp, Met
W09967288-A1.	
29-DEC-1999.	
24-JUN-1999;	99WO-JP003360.
25-JUN-1998;	98JP-00178449.
(SUMU) SUMITOMO PHARM CO LTD.	
(ITOH//) ITOH K.	
Itch K, Gomi S;	
WPI; 2000-116932/10.	
Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.	
Claim 10; Page 59; 64pp; Japanese.	
This sequence represents a cyclophilin B peptide of the invention. The peptides are tumor antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours	
Sequence 9 AA;	
Query Match	73.5%; Score 36; DB 3; Length 9;
Best Local Similarity	87.5%; Pred No. 1.4e+06;
Matches 7; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
1 KFHRYIKD 8	
1 KXHRVYKD 8	
RESULT 10	
AA69959	
AA69959	standard; peptide; 9 AA.
AA69959;	
11-APR-2000	(first entry)
Human cyclophilin B peptide fragment #39.	
Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.	
Homo sapiens.	
W09967288-A1.	

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PD      29-DEC-1999.
XX
PF      24-JUN-1999;    99WO-JP003360.
XX
PR      25-JUN-1998;    98JP-00178449.
XX
PA      (SUMU ) SUMITOMO PHARM CO LTD.
XX      (ITO//) ITOH K.
XX
PI      Itch K, Gomi S;
XX
DR      WPI; 2000-116932/10.
XX
PT      Tumor antigen peptides derived from cyclophilin B for treatment and
XX      diagnosis of tumors.
XX
PS      Claim 4; Page 61; 64pp; Japanese.
CC
XX      This sequence represents a cyclophilin B peptide of the invention. The
CC      peptides are tumour antigen peptides derived from cyclophilin B, that
CC      recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC      peptides are used for the treatment and diagnosis of tumours
XX
SQ      Sequence 9 AA;

Query Match          65.3%; Score 32; DB 3; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY      2 FHRVIXDP 9
        ||||| |
DB      2 FHRVIPSF 9

RESULT 11
ID      AAY69924
XX      AAY69924 standard; peptide; 11 AA.
XX
AC      AAY69924;
XX
DT      11-APR-2000 (first entry)
XX
DE      Human cyclophilin B peptide fragment #4.
XX
KW      Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
KW      HLA antigen; diagnosis; tumour; therapy.
XX
OS      Homo sapiens.
XX
PN      WO9967288-A1.
XX
PD      29-DEC-1999.
XX
PF      24-JUN-1999;    99WO-JP003360.
XX
PR      25-JUN-1998;    98JP-00178449.
XX
PA      (SUMU ) SUMITOMO PHARM CO LTD.
XX      (ITO//) ITOH K.
XX
PI      Itch K, Gomi S;
XX
DR      WPI; 2000-116932/10.
XX
PT      Tumor antigen peptides derived from cyclophilin B for treatment and
XX      diagnosis of tumors.
XX
PS      Claim 4; Page 50; 64pp; Japanese.
CC
XX      This sequence represents a cyclophilin B peptide of the invention. The
CC      peptides are tumour antigen peptides derived from cyclophilin B, that
CC      recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
CC      peptides are used for the treatment and diagnosis of tumours

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XX Sequence 11 AA;
SQ Query Match 65.3%; Score 32; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFHRYI 6
   |||||
   6 KFHRYI 11
DB

RESULT 12
AAR48203
ID AAR48203 standard; protein, 11 AA.
XX
AC AAR48203;
XX
XX 23-FEB-1994 (first entry)
XX
XX Human phospholipase A2 mature N-terminus.
XX
XX Human PLA2; insect cell; Baculovirus; preferred codon usage; codon bias;
XX increased recombinant protein expression; ds.
XX
XX Homo sapiens.
XX
XX JP05192167-A.
XX
XX 03-AUG-1993.
XX
XX 20-JAN-1992; 92JP-00028842.
XX
XX 20-JAN-1992; 92JP-00028842.
XX
XX 20-JAN-1992; 92JP-00028842.
XX
XX (YAMA) YAMANOUCHI PHARM CO LTD.
XX
XX WPI, 1993-277477/35.
XX
XX N-PSDB; AAQ48537; AAQ48538.
XX
XX DNA coding phospholipase A2 (PLA2) and prepn. - designed to match
XX frequency of using codon in insect cell.
XX
XX Claim 2 and 3; Page 2; 11pp; Japanese.
XX
XX A synthetic sequence coding for human pre-phospholipase A2 using codons
XX preferred for expression in insect cells is claimed. The synthetic DNA
XX fragment is used to produce a recombinant Baculovirus for infection of
XX insect cells. Human PLA2 having the mature N-terminal sequence of
XX AAR48203 can be produced by the transformants and readily purified
XX
XX Sequence 11 AA;
SQ Query Match 59.2%; Score 29; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 52;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIR 7
   |||||
   5 FHRVIR 10
DB

RESULT 13
AAP93365
ID AAP93365 standard; protein, 12 AA.
XX
XX AAP93365;
XX
XX 25-MAR-2003 (revised)
XX
XX 27-JUN-1980 (first entry)
XX
XX Amino acids encoded by oligonucleotide linker used to construct E. coli
XX human synovial phospholipase type A2 (sPLA2) expression vector p86-1A.

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XX Human synovial phospholipase A2; E. coli strain W3110 (ATCC 27325);
XX expression vector p86-1A; oligonucleotide linker.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Peptide 1..3
XX Protein 4..12
XX
XX WO8901773-A.
XX
XX 09-MAR-1989.
XX
XX 23-AUG-1988; 88WO-US002896.
XX
XX 27-AUG-1987; 87US-00089883.
XX
XX 06-JUL-1988; 88US-00215726.
XX
XX 16-AUG-1988; 88US-00231865.
XX
XX (BIOT-) BIOTECHN RES PARTN.
XX (UTOR) UNIV OF TORONTO INNOVAT.
XX
XX Johnson LK, Seilhamer J, Pruzanski W, Vadas P;
XX
XX WPI, 1989-085394/11.
XX
XX N-PSDB; AAN91261.
XX
XX Mammalian synovial phospholipase A2 - used in food processing, design and
XX screening of inflammation inhibitors, as an anticancer drug or vaccine
XX adjuvant etc.
XX
XX Disclosure; Fig 8; 70pp; English.
XX
XX It is encoded by the 'N-terminal hookup', having vector encoded residues
XX to its N-terminus and RASP residues to its C-terminus. A single base
XX change at the C-terminus of the sPLA2 gene created a HindIII site.
XX Digestion of this mutagenised clone with BclI and HindIII yielded a 370bp
XX fragment containing the entire sPLA2 coding region with the exception of
XX the first nine amino acid residues of the mature protein. These nine
XX residues, along with a cleavable fusion site (TTP) and an EcoRI site were
XX replaced with the oligonucleotide linker which encodes this sequence
XX (AAN91261) and another oligonucleotide linker (AAN91262). The two linkers
XX and the 370bp sPLA2 fragment were ligated into expression vector pHPF86
XX which consists of a pBR322 backbone, the E. coli T7P promoter, an RBS,
XX sequences encoding the amino terminal portion of the E. coli beta-
XX galactosidase gene followed by six T7P residues, EcoRI and HindIII sites,
XX and two strong E. coli transcription termination signals. This expression
XX construct was called p86-1A. It was used to transform E. coli strain W3110
XX (ATCC 27325) to produce sPLA2 as a fusion protein with beta-
XX galactosidase. (Updated on 25-MAR-2003 to correct PR field.) (Updated on
XX 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
XX field.)
XX
XX Sequence 12 AA;
SQ Query Match 59.2%; Score 29; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIR 7
   |||||
   6 FHRVIR 11
DB

RESULT 14
AAR69271
ID AAR69271 standard; peptide, 13 AA.
XX
XX AAR69271;
XX
XX 17-JUN-1995 (first entry)
XX

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XX Phospholipase A2 inhibiting peptide.
XX Antinflammatory; phospholipase A2; PLA2; inhibitor; heparin.
XX OS Synthetic.
XX FN Jp06263796-A.
XX PD 20-SEP-1994.
XX PF 12-MAR-1993; 93JP-00052012.
XX PR 12-MAR-1993; 93JP-00052012.
XX PA (TEIJ ) TEIJIN LTD.
XX WP1; 1994-338301/42.
XX New peptide which inhibits phospholipase - useful as antiinflammatory agent.
XX PS Example 1; Page 4; 5pp; Japanese.
XX The sequence is the only specific example of a generically claimed group
XX of peptides which inhibit phospholipase A2 associated with local
XX inflammation, or which inhibit binding thereof with heparin, and which
XX therefore are expected to be useful as antiinflammatory agents. The
XX generic peptides are of formula: A1-M1-M2-A2-M3-B1-B2-M4-M5-B3-M6-A3-X,
XX where A1, A2, A3 = Ser, Thr, Tyr, Asn, Gln, Asp, Glu, Arg or Lys; B1, B2,
XX B3 = His, Lys or Arg; M1, M2, M3, M4, M5, M6 = Leu, Val, Ile, Phe, Tyr,
XX Trp, Met, Gly or Ala; and X = a peptide composed of 1-3 amino acid
XX residues. Pref M1, M2, M4 and M5 = Leu, Ile, Val or Met; M3 = Phe, Tyr or
XX Trp; A1 and A2 = Asn, Ser or Thr; and X = a peptide of one or two amino
XX acids selected from Cys, Thr, Ser, Asp, Glu, Ala and Gly; one or more
XX amino acid residues may be substituted, deleted and/or inserted; and when
XX X = Cys, two of the Cys group may be connected to form a dimer
XX
XX Sequence 13 AA:
SQ
Query Match 59.2%; Score 29; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0.
QY 2 FHRVIX 7
Db 5 FHRMIK 10
|||||
|||||
RESULT 15
AAMS8475
ID AAMS8475 standard; peptide; 14 AA.
XX AAMS8475;
XX
XX 17-AUG-1998 (first entry)
XX
XX Human Type II PLA2 peptide residues 1-14.
XX
XX Human; PLA2; phospholipase A2; binding peptide; three-dimensional; 3D;
XX inhibitor; synovial fluid; septic shock; rheumatoid arthritis;
XX inflammatory disease.
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX WO9813376-A1.
XX
XX 02-APR-1998.
XX
XX 29-SEP-1997; 97WO-AU000648.
XX
XX 27-SEP-1996; 96AU-00002660.
XX PR 27-SEP-1996; 96AU-00002661.

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PA	(GARV-) GARVAN INST MEDICAL RES.
XX	
PI	Bryant K, Church WB, Inglis A, Scott K, Teeng A;
XX	
DR	WPI; 1998-230630/20.
XX	
PT	New non-peptide compounds that bind to and inhibit phospholipase A2,
PT	especially D-amino acid analogues of peptide(s) - are used to treat
PT	septic shock, rheumatoid arthritis and other inflammatory disease.
XX	
PS	Example; Page 21; 56pp; English.
XX	
CC	The present sequence represents a peptide from human type II PLA2
CC	(phospholipase A2) residues 1-14, used in an example of the present
CC	invention. The present invention describes non-peptide structures (i.e. a
CC	structure not composed exclusively of natural amino acids connected by
CC	amide bonds) having a conformation and polarity such that they bind to
CC	(1) at least 1 amino acid (aa) in the N-terminal helix of PLA2 and/or
CC	(preferably and) (11) at least 1 aa in the 70-77 aa region of PLA2.
CC	Binding of the non-peptide structure inhibits enzymatic activity of PLA2.
CC	The non-peptide structure binds to at least 1 (preferably 2) of residues
CC	N1, V3, M4, H6, R7, K10 and I12 in the N-terminal helix of PLA2, and
CC	particularly have the same spatial geometry and polarity as the peptide
CC	FLSYK (see AAm5474) in a conformation that allows it to bind to (1) at
CC	least 1 of the specified N-terminal helix aa and (2) at least 1 of aa 70-
CC	77. Especially this spatial geometry is defined by the hydrogen-bonding
CC	network between backbone residues of FLSYK and aa 1, 3, 4, 7 and 72-75 of
CC	PLA2. Non-peptide structures and peptide inhibitors of PLA2 are used to
CC	treat septic shock, rheumatoid arthritis and/or other inflammatory
CC	diseases. Inhibitors based on D-aa have longer in vivo half-lives than
CC	those based on L-aa, but have about the same inhibitory activity
XX	
SQ	Sequence 14 AA;
XX	
QY	2 FHRVIX 7
DB	5 FHRMIX 10
XX	
RESULT 16	
ADD84475	
ID	ADD84475 standard; peptide; 14 AA.
XX	
AC	ADD84475;
XX	
XX	29-JAN-2004 (first entry)
DT	
DE	121P1F1 modulating CTL epitope peptide #1029.
XX	
XX	121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic;
KW	gene therapy; vaccine; cancer; immune response; immunisation.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
PN	WO200295009-A2.
XX	
PD	28-NOV-2002.
XX	
PT	28-FEB-2002; 2002WO-US006242.
XX	
PR	05-MAR-2001; 2001US-00799250.
XX	
PA	(AGEN-) AGENSYS INC.
XX	
PI	Challita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
XX	Jakovovits A;
XX	

DR WPI; 2003-156757/15.

XX Composition comprising a substance that modulates the status of 121P1F1,
PT useful in diagnosing, preventing, prognosticating or treating patients
PT with cancer that expresses 121P1F1, such as breast, colon, ovarian or
XX lung cancer.

PS Claim 21; Page 239; 285pp; English.

XX The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121P1F1 (gene and encoded protein), or a
CC molecule that is modulated by 121P1F1, where the status of a cell that
CC expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121P1F1,
CC such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121P1F1 genes, as coding sequences for directing the
CC expression of 121P1F1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121P1F1 genes. The present sequence is used
CC in the exemplification of the present invention.

XX Sequence 14 AA;

SQ
Query Match 59.2%; Score 29; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 FHRVYIKDF 9
||:|:|:|:
DB 4 FHEIRIKSY 11

RESULT 17

AAR96521
ID AAR96521 standard; peptide; 10 AA.

XX AAR96521;

DT 07-MAR-1997 (first entry)

XX Hepatitis C virus type 9 peptide.

XX Hepatitis C virus; subtype; polymerase chain reaction; amplification;
XX PCR; primer; probe; antibody; infection.

OS Synthetic.

XX WO9613590-A2.

PN 09-MAY-1996.

XX 23-OCT-1995; 95WO-EP004155.

XX 21-OCT-1994; 94EP-00870166.

XX 28-JUN-1995; 95EP-00870076.

XX (INNO-) INNOGENETICS NV.

XX Maertens G, Stuyver L;

XX WPI; 1996-251460/25.

XX Hepatitis C virus poly-nucleic acid unique to unidentified sub-type -
PT used to develop probes and primers for new sub-types and vaccines to
PT prevent and treat infection.

XX Claim 5; Page 68; 150pp; English.

XX The peptides AAR96424-R96524 represent novel peptides derived from the

CC novel hepatitis C virus subtypes 1d-f, 2e-i, 2x, 2l, 3g, 4k-m, 7a-c or
CC types 9, 10 or 11 (see AAT7937-T7989). The sequences corresp. to the 5'
CC untranslated region (UR), the Core/E1, NS4 or NS5B regions of the genome.
CC This sequence is from the HCV subtype 9. The new HCV types were isolated
CC from patients with chronic HCV from the Benelux countries, France, the
CC Cameroon and Vietnam, because of their aberrant reactivities. The RNA was
CC extracted, cDNA synthesised and PCR amplified, cloned and genotyped. The
CC 5'UR, Core/E1 and NS5B regions were sequenced either directly or
CC partially and used to classify the new viruses into (sub)types based on
CC comparison with known sequences. The nucleotide sequences can be used to
CC synthesise probes and primers for the detection of HCV in a sample. The
CC polypeptides can be used to detect anti-HCV antibodies, for HCV typing or
CC to prevent HCV infections

XX Sequence 10 AA;

SQ
Query Match 55.1%; Score 27; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 KFRVYIKD 8
||:|:|:|:
DB 3 KXHYOTQD 10

RESULT 18

AAB82292
ID AAB82292 standard; peptide; 11 AA.

XX AAB82292;

DT 09-JUL-2001 (first entry)

XX Phosphorylation site in potato HMGR-CoA reductase.

XX 3-Hydroxy-3-methylglutaryl-CoA reductase; HMGR-CoA reductase; HMGR;
XX phosphorylation; isoprenoid; sterol; transgenic plant; potato;
XX pathogen resistance; disease resistance; crop protection.

XX Solanum tuberosum.

OS Solanum tuberosum.

XX Key

XX Modified-site 7 Location/Qualifiers

XX WO200131043-A1.

XX 03-MAY-2001.

XX 27-OCT-2000; 2000WO-GB004141.

XX 27-OCT-1999; 99GB-00025453.

XX (UYBR-) UNIV BRISTOL.

XX Halford NG, Hey SJ, Beale MH;

XX WPI; 2001-308654/32.

XX Modified 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene, useful for
PT generating transgenic plants having increased isoprenoid production,
PT comprising a modified phosphorylation site.

XX Claim 16; Page 18; 23pp; English.

XX The present sequence is that of a phosphorylated region of the 3-hydroxy-
CC 3-methylglutaryl-coenzyme A reductase (HMGR) protein of potato. The
CC invention relates to modified HMGR genes useful for generating transgenic
CC plants having increased isoprenoid (especially sterol) production. The
CC modified genes encode modified HMGR proteins, in which a phosphorylation
CC site has been rendered inactive by replacing a Ser, Thr or Tyr residue
CC with Ala or other amino acid residue. This reduces transcriptional
CC regulation. The HMGR genes may be in the form of mutant plant and

CC plant/non-plant or different plant chimeric genes. Transcriptional
CC regulation can also be avoided by using heterologous promoters. Increased
CC seed sterol content has been demonstrated in transgenic plants. The
CC invention is used to produce plants having increased insect and mite pest
CC resistance, particularly against species of Homoptera, Diptera,
CC Lepidoptera, Coleoptera, Hymenoptera, Hemiptera, Dictyoptera, Orthoptera,
CC arachnids and mites, or it is used to attract beneficial insects,
CC including Odonata, Hymenoptera, Coleoptera, Neuroptera, or arachnids or
CC mites to the plant. It is also used to produce plants having increased
CC pathogen resistance, particularly against a fungus, especially Fusarium,
CC Aspergillus, Phytophthora, Gaeumannomyces, Downy mildews, Colletotrichum,
CC Cochliobolus, Tapesia, Magnaporthe, Stagonospora, Rhynchosporium,
CC Septoria, Helminthosporium, and powdery mildews such as Blumeria and
CC Erysiphe. The modified genes are particularly useful in maize, wheat,
CC rice, barley, oilseed rape, beans, sunflower, cabbage, potato, spinach,
CC broccoli, pea, cauliflower, tomato, forest trees, roses and tea. The
CC invention may also be used to add nutritional benefit such as fat-soluble
CC vitamins E and K, and sterols to a crop plant

SQ Sequence 11 AA;

Query Match 55.1%; Score 27; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFHRYIKD 8
|:|:|:|
Db 3 KYNSIKD 10

RESULT 19
AAW92359
ID AAW92359 standard; peptide; 12 AA.

XX AAW92359;

DT 13-APR-1999 (first entry)

XX CYP2B1 immunogenic peptide.

XX Cytochrome P450; CYP2B1; immunogen; antibody; identification; therapy;

KM drug metabolism; inhibitor.

XX Synthetic.

OS US5866688-A.

PN 02-FEB-1999.

XX 02-FEB-1999.

XX 06-JUN-1995; 95US-00471286.

XX 06-JUN-1995; 95US-00471286.

XX (OXFO-) OXFORD BIOMEDICAL RES INC.

XX Kim EY, Putt DA, Kim H, Charnecki J;

XX WPI; 1999-142014/12.

XX Production of antibodies to Cytochrome P450 proteins - using a peptide

XX immunogen.

XX Claim 3; Col 5; 15pp; English.

CC This sequence represents an immunogenic peptide designed to raise
CC antibodies against the cytochrome P450 2B subfamily protein CYP2B1. This
CC peptide is used in a method for producing form-specific and/or inhibitory
CC antibodies against cytochrome P450 proteins that comprises determining
CC the amino acid sequence of the protein, aligning the desired amino acid
CC sequence with a comparison sequence, using an alignment algorithm, in
CC which the comparison sequence has been analysed by X-ray crystallography
CC or NMR, and where domains of the sequence comprise a substrate

CC recognition site, selecting a peptide sequence corresponding to a region
CC of a substrate recognition site (SRS) preparing a peptide having the
CC selected sequence and using the peptide as an immunogen. The antibodies
CC can be used as analytical tools to identify cytochrome P450 proteins
CC which are involved in the metabolism of drugs and physiological
CC substances. They may also be used as therapeutic agents to inhibit
CC specific cytochrome P450 proteins

SQ Sequence 12 AA;

Query Match 55.1%; Score 27; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVYIKD 8
|:|:|:|
Db 7 HRVYIKD 12

RESULT 20
AAW97263
ID AAW97263 standard; peptide; 14 AA.

XX AAW97263;

DT 24-JAN-2002 (first entry)

XX Human peptide #538 encoded by a SNP oligonucleotide.

XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KM complement related protein; cytochrome; kinesin; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
XX nervous system disease.

XX Homo sapiens.

OS W0200147944-A2.

PN 05-JUL-2001.

XX 28-DEC-2000; 2000WO-US035498.

XX 28-DEC-1999; 95US-0173419P.

XX 27-DEC-2000; 2000US-00173419.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-465210/50.

XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.

PS Disclosure; Page 3785; 4143pp; English.

CC The present invention relates to oligonucleotides (see AAU26793-AAU24659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interleukins, interferons, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid

CC arthritis, multiple sclerosis, diabetes, systemic lupus erythromatosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX

SO Sequence 14 AA;
Query Match 55.1%; Score 27; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 FHRVIXDP 9
| | | | |
| | | | |
DB 1 FARWIKER 8

RESULT 21
ABG94771
ID ABG94771 standard; peptide, 9 AA.
XX ABG94771;
XX

DT 02-DEC-2002 (first entry)

XX Replikin sequence identified by the 3-point recognition method #44.

XX Replikin; glioma; malignant; anthrax; small pox; antiviral; antibacterial;
XX 3-point-recognition; vaccine; immunogen; lethal Factor Protein pX01-107;
XX Surface Antigen S Precursor Protein.

XX Polyoma virus.

XX US2002120106-A1.

XX 29-AUG-2002.

XX 26-OCT-2001; 2001US-00984056.

XX 04-SEP-1998; 98US-00146755.

XX 27-MAR-2001; 2001US-00817144.

XX 27-MAR-2001; 2001US-0278761P.

XX 09-JUL-2001; 2001US-0303396P.

XX (BOGO/) BOGGOCH S.

XX (BOGO/) BOGGOCH E. S.

XX Bogoch S, Bogoch ES;

XX WPI; 2002-691212/74.

XX Disclosure; Page 3; 16pp; English.

XX The invention relates to isolated Bacillus anthracis and small pox virus
XX peptides, also known as replikins, comprising 7 to 50 amino acids
XX including at least one lysine residue located six to ten residues from a
XX second lysine residue, at least one histidine residue, and at least 6%
XX lysine residues. The peptides were identified using the 3-point-
XX recognition method and based on the replikin sequence isolated from
XX glioblastoma cells malignant peptide which is of non-human origin. Also
XX included are anti-replikin antibodies (or antibody cocktail), a method of
XX stimulating the immune system of a subject to produce antibodies to
XX Bacillus anthracis or small pox comprising administering an effective
XX amount of at least one or more Bacillus anthracis or small pox replikin
XX and an antisense nucleic acid molecule complementary to a mRNA encoding a
XX Bacillus anthracis polypeptide (e.g. Anthrax lethal Factor Protein pX01-
XX 107) comprising a replikin sequence, an antisense nucleic acid molecule
XX complementary to a mRNA encoding a small pox virus polypeptide (e.g.
XX Surface Antigen S Precursor Protein comprising a replikin sequence. The
XX peptides are useful for stimulating the immune system of a subject to

CC produce antibodies that bind specifically to Anthrax or small pox
CC polypeptides containing a replikin sequence. The peptides are useful for
CC generating antibodies that can be used in the treatment and/or prevention
CC of anthrax or small pox. The peptides are also useful for formulating
CC vaccines for treating anthrax or small pox. The present sequence is a
CC replikin sequence isolated by the 3-point-recognition system and sharing
CC structural similarity with the replikin sequence isolated from
CC glioblastoma cells malignant
XX

SO Sequence 9 AA;

Query Match 53.1%; Score 26; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.4e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KFRVIXKD 8
| | | | |
| | | | |
DB 1 KQREKMD 8

RESULT 22
ABG94772
ID ABG94772 standard; peptide, 9 AA.
XX ABG94772;
XX

DT 02-DEC-2002 (first entry)

XX Replikin sequence identified by the 3-point recognition method #45.

XX Replikin; glioma; malignant; anthrax; small pox; antiviral; antibacterial;
XX 3-point-recognition; vaccine; immunogen; lethal Factor Protein pX01-107;
XX Surface Antigen S Precursor Protein.

XX Polyoma virus.

XX US2002120106-A1.

XX 29-AUG-2002.

XX 26-OCT-2001; 2001US-00984056.

XX 04-SEP-1998; 98US-00146755.

XX 27-MAR-2001; 2001US-00817144.

XX 27-MAR-2001; 2001US-0278761P.

XX 09-JUL-2001; 2001US-0303396P.

XX (BOGO/) BOGGOCH S.

XX (BOGO/) BOGGOCH E. S.

XX Bogoch S, Bogoch ES;

XX WPI; 2002-691212/74.

XX Disclosure; Page 3; 16pp; English.

XX The invention relates to isolated Bacillus anthracis and small pox virus
XX peptides, also known as replikins, comprising 7 to 50 amino acids
XX including at least one lysine residue located six to ten residues from a
XX second lysine residue, at least one histidine residue, and at least 6%
XX lysine residues. The peptides were identified using the 3-point-
XX recognition method and based on the replikin sequence isolated from
XX glioblastoma cells malignant peptide which is of non-human origin. Also
XX included are anti-replikin antibodies (or antibody cocktail), a method of
XX stimulating the immune system of a subject to produce antibodies to
XX Bacillus anthracis or small pox comprising administering an effective
XX amount of at least one or more Bacillus anthracis or small pox replikin
XX and an antisense nucleic acid molecule complementary to a mRNA encoding a
XX Bacillus anthracis polypeptide (e.g. Anthrax lethal Factor Protein pX01-

107) comprising a replikin sequence, an antisense nucleic acid molecule complementary to a mRNA encoding a small pox virus polypeptide (e.g. Surface Antigen S Precursor Protein comprising a replikin sequence. The peptides are useful for stimulating the immune system of a subject to produce antibodies that bind specifically to Anthrax or small pox polypeptides containing a replikin sequence. The peptides are useful for generating antibodies that can be used in the treatment and/or prevention of anthrax or small pox. The peptides are also useful for formulating vaccines for treating anthrax or small pox. The present sequence is a replikin sequence isolated by the 3-point-recognition system and sharing structural similarity with the replikin sequence isolated from glioblastoma cells malignin

Sequence 9 AA;

Query Match 53.1%; Score 26; DB 5; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFHRYIKD 8

Db 1 KOHRELKD 8

RESULT 23

ABUS7321 ID ABUS7321 standard; peptide; 9 AA.

AC ABUS7321;

DT 08-APR-2003 (first entry)

DE Replikin peptide sequence #61.

KM Replikin; immunostimulant; vaccine; recognin.

OS Polymavirus sp.

XX US2002151677-A1.

PD 17-OCT-2002.

PF 26-OCT-2001; 2001US-00984057.

PR 27-MAR-2001; 2001US-0278761P.

PR 09-JUL-2001; 2001US-0303396P.

PA (BOGO/) BOGOGCH S.

PA (BOGO/) BOGOGCH E S.

PI Bogoch S, Bogoch ES;

DR WPI; 2003-182530/18.

XX New replikins or recognin peptides, useful for stimulating the immune system, and for targeting, labeling or destroying replikin-containing organisms.

PT Claim 78; Page 3; 17pp; English.

XX The invention describes an isolated replikin or recognin peptide (I)

CC comprising 7-50 amino acids including at least one lysine residue located 6 to 10 residues from a second lysine residue, at least one histidine residue and at least 6% lysine residues. The peptides are useful for stimulating the immune system, and for targeting, labeling or destroying replikin-containing organisms. The computer-readable mediums are useful for identifying a protein or peptide containing a replikin or recognin sequence. This is the amino acid sequence of a replikin peptide identified in the invention

CC Sequence 9 AA;

XX Query Match

53.1%; Score 26; DB 6; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFHRYIKD 8

Db 1 KOHRELKD 8

RESULT 24

ABUS7322 ID ABUS7322 standard; peptide; 9 AA.

AC ABUS7322;

DT 08-APR-2003 (first entry)

DE Replikin peptide sequence #62.

KM Replikin; immunostimulant; vaccine; recognin.

OS Polymavirus sp.

XX US2002151677-A1.

PD 17-OCT-2002.

PF 26-OCT-2001; 2001US-00984057.

PR 27-MAR-2001; 2001US-0278761P.

PR 09-JUL-2001; 2001US-0303396P.

PA (BOGO/) BOGOGCH S.

PA (BOGO/) BOGOGCH E S.

PI Bogoch S, Bogoch ES;

DR WPI; 2003-182530/18.

XX New replikins or recognin peptides, useful for stimulating the immune system, and for targeting, labeling or destroying replikin-containing organisms.

PT Claim 79; Page 3; 17pp; English.

XX The invention describes an isolated replikin or recognin peptide (I)

CC comprising 7-50 amino acids including at least one lysine residue located 6 to 10 residues from a second lysine residue, at least one histidine residue and at least 6% lysine residues. The peptides are useful for stimulating the immune system, and for targeting, labeling or destroying replikin-containing organisms. The computer-readable mediums are useful for identifying a protein or peptide containing a replikin or recognin sequence. This is the amino acid sequence of a replikin peptide identified in the invention

CC Sequence 9 AA;

XX Query Match

53.1%; Score 26; DB 6; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.4e+06; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFHRYIKD 8

Db 1 KOHRELKD 8

RESULT 25

ADD82912 ID ADD82912 standard; peptide; 9 AA.

AC ADD82912;

DT 29-JAN-2004 (first entry)

XX

PA (AGEN-) AGENSYS INC.
XX
XX Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI Jakobovits A;
XX
XX WPI; 2003-156757/15.
DR
XX
XX Composition comprising a substance that modulates the status of 121PI1,
PT useful in diagnosing, preventing, prognosticating or treating patients
PI with cancer that expresses 121PI1, such as breast, colon, ovarian or
PT lung cancer.
PS
XX
XX Claim 21; Page 226; 285pp; English.
XX
XX The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121PI1 (gene and encoded protein), or a
CC molecule that is modulated by 121PI1, where the status of a cell that
CC expresses 121PI1 is modulated. The human 121PI1 gene maps to chromosome
CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121PI1,
CC such as breast, colon, ovarian or lung cancer. The 121PI1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121PI1 antibodies can be used in active or passive immunisation. 121PI1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121PI1 genes, as coding sequences for directing the
CC expression of 121PI1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121PI1 genes. The present sequence is used
CC in the exemplification of the present invention.
CC
XX
XX Sequence 9 AA;
SQ
Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 FHRIK 7
Db 1 FHRIK 6
RESULT 28
ADD84174
ID ADD84174 standard; peptide; 9 AA.
XX
XX ADD84174;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
DE 121PI1 modulating CTL epitope peptide #728.
XX
XX 121PI1; 121PI1 modulation; human; chromosome 4q; cytostatic;
KM gene therapy; vaccine; cancer; immune response; immunisation.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX WO200295009-A2.
FN
XX
XX 28-NOV-2002.
PD
XX
XX 28-FEB-2002; 2002WO-US006242.
PF
XX
XX 05-MAR-2001; 2001US-00799250.
PR
XX
XX (AGEN-) AGENSYS INC.
PA
XX Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI Jakobovits A;
XX
XX WPI; 2003-156757/15.
DR
XX
XX Composition comprising a substance that modulates the status of 121PI1,

PT useful in diagnosing, preventing, prognosticating or treating patients
PT with cancer that expresses 121PI1, such as breast, colon, ovarian or
PT lung cancer.
XX
XX Claim 21; Page 226; 285pp; English.
XX
XX The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121PI1 (gene and encoded protein), or a
CC molecule that is modulated by 121PI1, where the status of a cell that
CC expresses 121PI1 is modulated. The human 121PI1 gene maps to chromosome
CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121PI1,
CC such as breast, colon, ovarian or lung cancer. The 121PI1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121PI1 antibodies can be used in active or passive immunisation. 121PI1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121PI1 genes, as coding sequences for directing the
CC expression of 121PI1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121PI1 genes. The present sequence is used
CC in the exemplification of the present invention.
CC
XX
XX Sequence 9 AA;
SQ
Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 FHRIK 7
Db 1 FHRIK 6
RESULT 29
ADD83046
ID ADD83046 standard; peptide; 9 AA.
XX
XX ADD83046;
AC
XX
XX 29-JAN-2004 (first entry)
DT
XX
DE 121PI1 modulating CTL epitope peptide SEQ ID NO:905.
XX
XX 121PI1; 121PI1 modulation; human; chromosome 4q; cytostatic;
KM gene therapy; vaccine; cancer; immune response; immunisation.
XX
XX Synthetic.
OS
XX Homo sapiens.
OS
XX WO200295009-A2.
FN
XX
XX 28-NOV-2002.
PD
XX
XX 28-FEB-2002; 2002WO-US006242.
PF
XX
XX 05-MAR-2001; 2001US-00799250.
PR
XX
XX (AGEN-) AGENSYS INC.
PA
XX Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
PI Jakobovits A;
XX
XX WPI; 2003-156757/15.
DR
XX
XX Composition comprising a substance that modulates the status of 121PI1,
PT useful in diagnosing, preventing, prognosticating or treating patients
PT with cancer that expresses 121PI1, such as breast, colon, ovarian or
PT lung cancer.
PS
XX
XX Claim 21; SEQ ID NO 905; 285pp; English.
XX
XX The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121PI1 (gene and encoded protein), or a

molecule that is modulated by 121P1F1, where the status of a cell that expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome 4q. (1) Has cytostatic activity, and can be used in gene therapy, and in vaccines. The composition (I) can be used for diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its fragment can be used to elicit a humoral or cellular immune response. 121P1F1 antibodies are useful as probes and primers for the amplification or detection of 121P1F1 genes, as coding sequences for directing the expression of 121P1F1 polypeptides, or as tools for modulating or inhibiting the expression of 121P1F1 genes. The present sequence is used in the exemplification of the present invention.

Sequence 9 AA:

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIX 7
||:||||
Db 4 FHEIIX 9

RESULT 30

ADD83134
ID ADD83134 standard; peptide; 9 AA.

AC ADD83134;

DT 29-JAN-2004 (first entry)

DE 121P1F1 modulating CTL epitope peptide SEQ ID NO:993.

KW 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic; gene therapy; vaccine; cancer; immune response; immunisation.

OS Synthetic.

PN Homo sapiens.

WO200295009-A2.

PD 28-NOV-2002.

PF 28-FEB-2002; 2002WO-US006242.

PR 05-MAR-2001; 2001US-00799250.

PA (AGEN-) AGENSYS INC.

PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W, Jakobovits A;

DR WPI; 2003-156757/15.

PT Composition comprising a substance that modulates the status of 121P1F1, useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer.

PS Claim 21; SEQ ID NO 993; 285bp; English.

CC The present invention describes a composition (I) comprising a substance that modulates the status of 121P1F1 (gene and encoded protein), or a molecule that is modulated by 121P1F1, where the status of a cell that expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome 4q. (1) Has cytostatic activity, and can be used in gene therapy, and in vaccines. The composition (I) can be used for diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its fragment can be used to elicit a humoral or cellular immune response. 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1

CC polynucleotides are useful as probes and primers for the amplification or detection of 121P1F1 genes, as coding sequences for directing the expression of 121P1F1 polypeptides, or as tools for modulating or inhibiting the expression of 121P1F1 genes. The present sequence is used in the exemplification of the present invention.

Sequence 9 AA:

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIX 7
||:||||
Db 1 FHEIIX 6

RESULT 31

ADD83215
ID ADD83215 standard; peptide; 9 AA.

AC ADD83215;

DT 29-JAN-2004 (first entry)

DE 121P1F1 modulating CTL epitope peptide SEQ ID NO:1074.

KW 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic; gene therapy; vaccine; cancer; immune response; immunisation.

OS Synthetic.

PN Homo sapiens.

WO200295009-A2.

PD 28-NOV-2002.

PF 28-FEB-2002; 2002WO-US006242.

PR 05-MAR-2001; 2001US-00799250.

PA (AGEN-) AGENSYS INC.

PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W, Jakobovits A;

DR WPI; 2003-156757/15.

PT Composition comprising a substance that modulates the status of 121P1F1, useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer.

PS Claim 21; SEQ ID NO 1074; 285bp; English.

CC The present invention describes a composition (I) comprising a substance that modulates the status of 121P1F1 (gene and encoded protein), or a molecule that is modulated by 121P1F1, where the status of a cell that expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome 4q. (1) Has cytostatic activity, and can be used in gene therapy, and in vaccines. The composition (I) can be used for diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its fragment can be used to elicit a humoral or cellular immune response. 121P1F1 antibodies are useful as probes and primers for the amplification or detection of 121P1F1 genes, as coding sequences for directing the expression of 121P1F1 polypeptides, or as tools for modulating or inhibiting the expression of 121P1F1 genes. The present sequence is used in the exemplification of the present invention.

Sequence 9 AA:

Query Match 53.1%; Score 26; DB 7; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIR 7
 ||:||||
 DB 1 FHEIRK 6

RESULT 32

ADD84124
 ID ADD84124 standard; peptide; 9 AA.

AC ADD84124;

XX 29-JAN-2004 (first entry)

DE 121PIFI modulating CTL epitope peptide #678.

XX 121PIFI; 121PIFI modulation; human; chromosome 4q; cytostatic;
 KW gene therapy; vaccine; cancer; immune response; immunisation.

XX Synthetic.

OS Homo sapiens.

XX WO200295009-A2.

XX 28-NOV-2002.

XX 28-FEB-2002; 2002WO-US006242.

XX 05-MAR-2001; 2001US-00799250.

XX (AGEN-) AGENSYS INC.

PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
 FI Jakobovits A;

XX WPI; 2003-156757/15.

XX Composition comprising a substance that modulates the status of 121PIFI,
 PT useful in diagnosing, preventing, prognosticating or treating patients
 PT with cancer that expresses 121PIFI, such as breast, colon, ovarian or
 PT lung cancer.

XX Claim 21; Page 224; 285pp; English.

XX The present invention describes a composition (I) comprising a substance
 CC that modulates the status of 121PIFI (gene and encoded protein), or a
 CC molecule that is modulated by 121PIFI, where the status of a cell that
 CC expresses 121PIFI is modulated. The human 121PIFI gene maps to chromosome
 CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
 CC vaccines. The composition (I) can be used for diagnosing, preventing,
 CC prognosticating or treating patients with cancer that expresses 121PIFI,
 CC such as breast, colon, ovarian or lung cancer. The 121PIFI gene or its
 CC fragment can be used to elicit a humoral or cellular immune response.
 CC 121PIFI antibodies can be used in active or passive immunisation. 121PIFI
 CC polynucleotides are useful as probes and primers for the amplification or
 CC detection of 121PIFI genes, as coding sequences for directing the
 CC expression of 121PIFI polypeptides, or as tools for modulating or
 CC inhibiting the expression of 121PIFI genes. The present sequence is used
 CC in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIR 7
 ||:||||
 DB 3 FHEIRK 8

RESULT 33
 ADD84150
 ID ADD84150 standard; peptide; 9 AA.

XX ADD84150;

XX 29-JAN-2004 (first entry)

DE 121PIFI modulating CTL epitope peptide #704.

XX 121PIFI; 121PIFI modulation; human; chromosome 4q; cytostatic;
 KW gene therapy; vaccine; cancer; immune response; immunisation.

XX Synthetic.

OS Homo sapiens.

XX WO200295009-A2.

XX 28-NOV-2002.

XX 28-FEB-2002; 2002WO-US006242.

XX 05-MAR-2001; 2001US-00799250.

XX (AGEN-) AGENSYS INC.

PI Chailita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
 FI Jakobovits A;

XX WPI; 2003-156757/15.

XX Composition comprising a substance that modulates the status of 121PIFI,
 PT useful in diagnosing, preventing, prognosticating or treating patients
 PT with cancer that expresses 121PIFI, such as breast, colon, ovarian or
 PT lung cancer.

XX Claim 21; Page 225; 285pp; English.

XX The present invention describes a composition (I) comprising a substance
 CC that modulates the status of 121PIFI (gene and encoded protein), or a
 CC molecule that is modulated by 121PIFI, where the status of a cell that
 CC expresses 121PIFI is modulated. The human 121PIFI gene maps to chromosome
 CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
 CC vaccines. The composition (I) can be used for diagnosing, preventing,
 CC prognosticating or treating patients with cancer that expresses 121PIFI,
 CC such as breast, colon, ovarian or lung cancer. The 121PIFI gene or its
 CC fragment can be used to elicit a humoral or cellular immune response.
 CC 121PIFI antibodies can be used in active or passive immunisation. 121PIFI
 CC polynucleotides are useful as probes and primers for the amplification or
 CC detection of 121PIFI genes, as coding sequences for directing the
 CC expression of 121PIFI polypeptides, or as tools for modulating or
 CC inhibiting the expression of 121PIFI genes. The present sequence is used
 CC in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIR 7
 ||:||||
 DB 1 FHEIRK 6

RESULT 34

ADD83010
 ID ADD83010 standard; peptide; 9 AA.

XX ADD83010;

XX 29-JAN-2004 (first entry)

XX (AGEN-) AGENSYS INC.
PA Challita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
DR MPI; 2003-156757/15.

XX Composition comprising a substance that modulates the status of 121Pfl,
PT useful in diagnosing, preventing, prognosticating or treating patients
PR with cancer that expresses 121Pfl, such as breast, colon, ovarian or
PS lung cancer.
PP Claim 21; Page 227; 285pp; English.

XX The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121Pfl (gene and encoded protein), or a
CC molecule that is modulated by 121Pfl, where the status of a cell that
CC expresses 121Pfl is modulated. The human 121Pfl gene maps to chromosome
CC 4q. (It has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121Pfl,
CC such as breast, colon, ovarian or lung cancer. The 121Pfl gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121Pfl antibodies are useful in active or passive immunisation. 121Pfl
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121Pfl genes, as coding sequences for directing the
CC expression of 121Pfl polypeptides, or as tools for modulating or
CC inhibiting the expression of 121Pfl genes. The present sequence is used
CC in the exemplification of the present invention.

SQ Sequence 9 AA;

Query March 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred.No. 1.4e-06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0.

OY 2 FHRVIX 7
|||:
Db 3 FHEIKX 8

RESULT 37
ADD82989
ID ADD82989 standard; peptide; 9 AA.
AC ADD82989;
XX 29-JAN-2004 (first entry)
DT
DE 121Pfl modulating CTL epitope peptide SEQ ID NO:848.
XX
DM 121Pfl; 121Pfl modulation; human; chromosome 4q; cytosolic;
KM gene therapy; vaccine; cancer; immune response; immunisation.
XX Synthetic.
OS Homo sapiens.
XX WO200295009-A2.
XX
XX 28-NOV-2002.
PD
XX 28-FEB-2002; 2002WO-US006242.
PF
XX 05-MAR-2001; 2001US-00799250.
PR
XX (AGEN-) AGENSYS INC.
PA
XX Challita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
PI Jakobovits A;
XX
XX MPI; 2003-156757/15.
XX

PT Composition comprising a substance that modulates the status of 121P1F1,
 PT useful in diagnosing, preventing, prognosticating or treating patients
 PT with cancer that expresses 121P1F1, such as breast, colon, ovarian or
 PT lung cancer.
 PS
 PS Claim 21; SEQ ID NO 848; 285pp; English.
 XX
 CC The present invention describes a composition (I) comprising a substance
 CC that modulates the status of 121P1F1 (gene and encoded protein), or a
 CC molecule that is modulated by 121P1F1, where the status of a cell that
 CC expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
 CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
 CC vaccines. The composition (I) can be used for diagnosing, preventing,
 CC prognosticating or treating patients with cancer that expresses 121P1F1,
 CC such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
 CC fragment can be used to elicit a humoral or cellular immune response.
 CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
 CC polynucleotides are useful as probes and primers for the amplification or
 CC detection of 121P1F1 genes, as coding sequences for directing the
 CC expression of 121P1F1 polypeptides, or as tools for modulating or
 CC inhibiting the expression of 121P1F1 genes. The present sequence is used
 CC in the exemplification of the present invention.
 XX
 XX Sequence 9 AA:
 SQ
 Query Match 53.1%; Score 26; DB 7; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FHRYIX 7
 ||:||
 Db 1 FHEIIX 6
 RESULT 38
 ID ADD83208
 ID ADD83208 standard; peptide; 9 AA.
 XX ADD83208;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE 121P1F1 modulating CTL epitope peptide SEQ ID NO:1067.
 XX
 KW 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic;
 KW gene therapy; vaccine; cancer; immune response; immunisation.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO200295009-A2.
 PN
 PD 28-NOV-2002.
 PD
 PF 28-FEB-2002; 2002WC-US006242.
 PF
 PR 05-MAR-2001; 2001US-00799250.
 PR
 PA (AGEN-) AGENSYS INC.
 PA
 PI Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
 PI Jakobovits A;
 PI
 DR WPI; 2003-156757/15.
 DR
 CC Composition comprising a substance that modulates the status of 121P1F1,
 CC useful in diagnosing, preventing, prognosticating or treating patients
 CC with cancer that expresses 121P1F1, such as breast, colon, ovarian or
 CC lung cancer.
 PS
 PS Claim 21; SEQ ID NO 1067; 285pp; English.
 XX
 CC The present invention describes a composition (I) comprising a substance

CC that modulates the status of 121P1F1 (gene and encoded protein), or a
CC molecule that is modulated by 121P1F1, where the status of a cell that
CC expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
CC 4q. (1) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121P1F1,
CC such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121P1F1 genes, as coding sequences for directing the
CC expression of 121P1F1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121P1F1 genes. The present sequence is used
CC in the exemplification of the present invention.

CC
XX
SQ Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 FHRV1K 7
||:|
Db 2 FHE1IK 7

RESULT 39
ADD82979
ID ADD82979 standard; peptide; 9 AA.

XX
XX
AC ADD82979;
XX
XX
DT 29-JAN-2004 (first entry)
XX
XX
DE 121P1F1 modulating CTL epitope peptide SEQ ID NO:838.

XX
XX
KW 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic;
XX gene therapy; vaccine; cancer; immune response; immunisation.

XX
OS Synthetic.
XX Homo sapiens.

XX
PN WO200295009-A2.

XX
XX
PD 28-NOV-2002.

XX
XX
PF 28-FEB-2002; 2002WO-US006242.

XX
XX
PR 05-MAR-2001; 2001US-00799250.

XX
XX
PA (AGEN-) AGENSYS INC.

XX
XX
PI Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
XX Jakobovits A;

XX
XX
PI WPI; 2003-156757/15.

XX
XX
PT Composition comprising a substance that modulates the status of 121P1F1,
XX useful in diagnosing, preventing, prognosticating or treating patients
XX with cancer that expresses 121P1F1, such as breast, colon, ovarian or
XX lung cancer.

XX
XX
PS Claim 21; SEQ ID NO 838; 285bp; English.

XX
XX
CC The present invention describes a composition (I) comprising a substance
XX that modulates the status of 121P1F1 (gene and encoded protein), or a
XX molecule that is modulated by 121P1F1, where the status of a cell that
XX expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
XX 4q. (1) has cytostatic activity, and can be used in gene therapy, and in
XX vaccines. The composition (I) can be used for diagnosing, preventing,
XX prognosticating or treating patients with cancer that expresses 121P1F1,
XX such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
XX fragment can be used to elicit a humoral or cellular immune response.

CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121P1F1 genes, as coding sequences for directing the
CC expression of 121P1F1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121P1F1 genes. The present sequence is used
CC in the exemplification of the present invention.

CC
XX
SQ Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 FHRV1K 7
||:|
Db 4 FHE1IK 9

RESULT 40
ADD83263
ID ADD83263 standard; peptide; 9 AA.

XX
XX
AC ADD83263;
XX
XX
DT 29-JAN-2004 (first entry)
XX
XX
DE 121P1F1 modulating CTL epitope peptide SEQ ID NO:1122.

XX
XX
KW 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic;
XX gene therapy; vaccine; cancer; immune response; immunisation.

XX
OS Synthetic.
XX Homo sapiens.

XX
PN WO200295009-A2.

XX
XX
PD 28-NOV-2002.

XX
XX
PF 28-FEB-2002; 2002WO-US006242.

XX
XX
PR 05-MAR-2001; 2001US-00799250.

XX
XX
PA (AGEN-) AGENSYS INC.

XX
XX
PI Chailita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;
XX Jakobovits A;

XX
XX
PI WPI; 2003-156757/15.

XX
XX
PT Composition comprising a substance that modulates the status of 121P1F1,
XX useful in diagnosing, preventing, prognosticating or treating patients
XX with cancer that expresses 121P1F1, such as breast, colon, ovarian or
XX lung cancer.

XX
XX
PS Claim 21; SEQ ID NO 1122; 285bp; English.

XX
XX
CC The present invention describes a composition (I) comprising a substance
XX that modulates the status of 121P1F1 (gene and encoded protein), or a
XX molecule that is modulated by 121P1F1, where the status of a cell that
XX expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
XX 4q. (1) has cytostatic activity, and can be used in gene therapy, and in
XX vaccines. The composition (I) can be used for diagnosing, preventing,
XX prognosticating or treating patients with cancer that expresses 121P1F1,
XX such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
XX fragment can be used to elicit a humoral or cellular immune response.
XX 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
XX polynucleotides are useful as probes and primers for the amplification or
XX detection of 121P1F1 genes, as coding sequences for directing the
XX expression of 121P1F1 polypeptides, or as tools for modulating or
XX inhibiting the expression of 121P1F1 genes. The present sequence is used
XX in the exemplification of the present invention.

XX
XX
SQ Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVTK 7
||:|
1 FHEIHK 6

Db 1 FHEIHK 6

RESULT 41
ADD82850
ID ADD82850 standard; peptide; 9 AA.
XX
XX ADD82850;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX 121P1F1 modulating CTL epitope peptide SEQ ID NO:707.
DE
XX
XX 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic;
KM gene therapy; vaccine; cancer; immune response; immunisation.
XX
XX Synthetic.
OS Homo sapiens.
XX MO200295009-A2.
PN
XX 28-NOV-2002.
PD
XX 28-FEB-2002; 2002WO-US006242.
PF
XX 05-MAR-2001; 2001US-00799250.
PR
XX (AGEN-) AGENSYS INC.
PA
F1 Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
P1 Jakobovits A;
XX
XX WPI; 2003-156757/15.
DR
XX
XX Composition comprising a substance that modulates the status of 121P1F1,
PT useful in diagnosing, preventing, prognosticating or treating patients
PT with cancer that expresses 121P1F1, such as breast, colon, ovarian or
PT lung cancer.
PS Claim 21; SEQ ID NO 707; 285bp; English.
XX
XX The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121P1F1 (gene and encoded protein), or a
CC molecule that is modulated by 121P1F1, where the status of a cell that
CC expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121P1F1,
CC such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121P1F1 genes, as coding sequences for directing the
CC expression of 121P1F1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121P1F1 genes. The present sequence is used
CC in the exemplification of the present invention.
SQ Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVTK 7
||:|
3 FHEIHK 8

Db 3 FHEIHK 8

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVTK 7
||:|
3 FHEIHK 8

Db 3 FHEIHK 8

RESULT 42
ADD82866
ID ADD82866 standard; peptide; 9 AA.
XX
XX ADD82866;
AC
XX 29-JAN-2004 (first entry)
DT
XX
XX 121P1F1 modulating CTL epitope peptide SEQ ID NO:723.
DE
XX
XX 121P1F1; 121P1F1 modulation; human; chromosome 4q; cytostatic;
KM gene therapy; vaccine; cancer; immune response; immunisation.
XX
XX Synthetic.
OS Homo sapiens.
XX MO200295009-A2.
PN
XX 28-NOV-2002.
PD
XX 28-FEB-2002; 2002WO-US006242.
PF
XX 05-MAR-2001; 2001US-00799250.
PR
XX (AGEN-) AGENSYS INC.
PA
F1 Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W,
P1 Jakobovits A;
XX
XX WPI; 2003-156757/15.
DR
XX
XX Composition comprising a substance that modulates the status of 121P1F1,
PT useful in diagnosing, preventing, prognosticating or treating patients
PT with cancer that expresses 121P1F1, such as breast, colon, ovarian or
PT lung cancer.
PS Claim 21; SEQ ID NO 723; 285bp; English.
XX
XX The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121P1F1 (gene and encoded protein), or a
CC molecule that is modulated by 121P1F1, where the status of a cell that
CC expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121P1F1,
CC such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121P1F1 genes, as coding sequences for directing the
CC expression of 121P1F1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121P1F1 genes. The present sequence is used
CC in the exemplification of the present invention.
SQ Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVTK 7
||:|
2 FHEIHK 7

Db 2 FHEIHK 7

RESULT 43
ADD83127
ID ADD83127 standard; peptide; 9 AA.
XX
XX ADD83127;
AC
XX

Query Match 53.1%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVTK 7
||:|
2 FHEIHK 7

Db 2 FHEIHK 7

DT	29-JAN-2004	(first entry)	
XX			
DE	121P1F1	modulating CTL epitope peptide SEQ ID NO:986.	
XX			
KW	121P1F1; 121P1F1	modulation; human; chromosome 4q; cytostatic;	
KW	gene therapy; vaccine; cancer; immune response; immunisation.		
XX			
OS	Synthetic.		
XX	Homo sapiens.		
XX	MO200295009-A2.		
FN			
PD	28-NOV-2002.		
XX			
PF	28-FEB-2002; 2002WO-US006242.		
XX			
PR	05-MAR-2001; 2001US-00799250.		
XX			
PA	(AGEN-) AGENSYS INC.		
XX			
PI	Challita-Eid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W;		
PI	Jakovovits A;		
XX			
DR	WPI, 2003-156757/15.		
XX			
PT	Composition comprising a substance that modulates the status of 121P1F1,		
PT	useful in diagnosing, preventing, prognosticating or treating patients		
PT	with cancer that expresses 121P1F1, such as breast, colon, ovarian or		
PT	lung cancer.		
XX			
PS	Claim 21; SEQ ID NO 986; 285bp; English.		
XX			
CC	The present invention describes a composition (I) comprising a substance		
CC	that modulates the status of 121P1F1 (gene and encoded protein), or a		
CC	molecule that is modulated by 121P1F1, where the status of a cell that		
CC	expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome		
CC	4q. (I) has cytostatic activity, and can be used in gene therapy, and in		
CC	vaccines. The composition (I) can be used for diagnosing, preventing,		
CC	prognosticating or treating patients with cancer that expresses 121P1F1,		
CC	such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its		
CC	fragment can be used to elicit a humoral or cellular immune response.		
CC	121P1F1 antibodies can be used in active or passive immunisation. 121P1F1		
CC	polynucleotides are useful as probes and primers for the amplification or		
CC	detection of 121P1F1 genes, as coding sequences for directing the		
CC	expression of 121P1F1 polypeptides, or as tools for modulating or		
CC	inhibiting the expression of 121P1F1 genes. The present sequence is used		
CC	in the exemplification of the present invention.		
XX			
XX			
SO	Sequence 9 AA:		
XX			
Query Match	53.1%;	Score 26;	DB 7; Length 9;
Best Local Similarity	66.7%;	Pred. No. 1.4e+06;	
Matches 4; Conservative	1;	Mismatches 1;	Indels 0; Gaps 0;
QY	2 FHRVIX 7		
	:		
Db	3 FHEIIX 8		
XX			
RESULT 44			
ID	ADD83203		
XX	ADD83203 standard; peptide; 9 AA.		
AC	ADD83203;		
XX			
DT	29-JAN-2004 (first entry)		
XX			
DE	121P1F1	modulating CTL epitope peptide SEQ ID NO:1062.	
XX			
KW	121P1F1; 121P1F1	modulation; human; chromosome 4q; cytostatic;	
KW	gene therapy; vaccine; cancer; immune response; immunisation.		
XX			
OS	Synthetic.		

XX	OS	Homo sapiens.
XX	PV	WO200295009-A2.
XX	PD	
XX	PP	28-NOV-2002.
XX	PR	28-FEB-2002; 2002WO-US006242.
XX	PI	05-MAR-2001; 2001US-00799250.
XX	PA	(AGEN-) AGENSYS INC.
XX	PI	Challita-Bid PM, Hubert RS, Raitano AB, Faris M, Afar DEH, Ge W, Jakobovits A;
XX	DR	WPI; 2003-156757/15..
PT	PT	Composition comprising a substance that modulates the status of 121P1F1,
PT	PT	useful in diagnosing, preventing, prognosticating or treating patients with cancer that expresses 121P1F1, such as breast, colon, ovarian or lung cancer.
XX	PS	Claim 21; SEQ ID NO 1062; 285bp; English.
XX	CC	The present invention describes a composition (I) comprising a substance
CC	CC	that modulates the status of 121P1F1 (gene and encoded protein), or a
CC	CC	molecule that is modulated by 121P1F1, where the status of a cell that
CC	CC	expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
CC	CC	4q. (i) has cytostatic activity, and can be used in gene therapy, and in
CC	CC	vaccines. The composition (I) can be used for diagnosing, preventing,
CC	CC	prognosticating or treating patients with cancer that expresses 121P1F1,
CC	CC	such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
CC	CC	fragment can be used to elicit a humoral or cellular immune response.
CC	CC	121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
CC	CC	polynucleotides are useful as probes and primers for the amplification or
CC	CC	detection of 121P1F1 genes, as coding sequences for directing the
CC	CC	expression of 121P1F1 polypeptides, or as tools for modulating or
CC	CC	inhibiting the expression of 121P1F1 genes. The present sequence is used
CC	CC	in the exemplification of the present invention.
XX	SQ	Sequence 9 AA:
XX	Query Match	53.1%; Score 26; DB 7; Length 9;
XX	Best Local Similarity	66.7%; Pred. No. 1.4e+06;
XX	Matches 4; Conservative	1; Mismatches 1; Indels 0; Gaps 0;
OY	2 FHRVIX 7	
	:	
DB	4 FHEIIX 9	
XX	RESULT 45	
XX	ADD84128	ADD84128 standard; peptide; 9 AA.
XX	AC	ADD84128;
XX	AD	29-JAN-2004 (first entry)
XX	DE	121P1F1 modulating CTL epitope peptide #682.
XX	KM	121P1F1; 121P1F1 modulation; human; chromosome 4q; cytosstatic; gene therapy; vaccine; cancer; immune response; immunisation.
XX	OS	Synthetic.
XX	OS	Homo sapiens.
XX	PN	WO200295009-A2.
XX	PD	28-NOV-2002.
XX	PF	28-FEB-2002; 2002WO-US006242.

PR 05-MAR-2001; 2001US-00799250.

XX (AGEN-) AGENSYS INC.

PA Challita-Bid PM, Hubert RS, Raitano AB, Farris M, Afar DEH, Ge W,
PI Jakovovits A;

XX WPI; 2003-156757/15.

DR
XX Composition comprising a substance that modulates the status of 121P1F1,
PT useful in diagnosing, preventing, prognosticating or treating patients
PT with cancer that expresses 121P1F1, such as breast, colon, ovarian or
XX lung cancer.

PS Claim 21; Page 224; 285pp; English.

CC The present invention describes a composition (I) comprising a substance
CC that modulates the status of 121P1F1 (gene and encoded protein), or a
CC molecule that is modulated by 121P1F1, where the status of a cell that
CC expresses 121P1F1 is modulated. The human 121P1F1 gene maps to chromosome
CC 4q. (I) has cytostatic activity, and can be used in gene therapy, and in
CC vaccines. The composition (I) can be used for diagnosing, preventing,
CC prognosticating or treating patients with cancer that expresses 121P1F1,
CC such as breast, colon, ovarian or lung cancer. The 121P1F1 gene or its
CC fragment can be used to elicit a humoral or cellular immune response.
CC 121P1F1 antibodies can be used in active or passive immunisation. 121P1F1
CC polynucleotides are useful as probes and primers for the amplification or
CC detection of 121P1F1 genes, as coding sequences for directing the
CC expression of 121P1F1 polypeptides, or as tools for modulating or
CC inhibiting the expression of 121P1F1 genes. The present sequence is used
CC in the exemplification of the present invention.

XX
SQ Sequence 9 AA;

Query Match 53.1%; Score 26; DB 7; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.4e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 FHRVIK 7
||:|

Db 1 PHEIK 6

Search completed: August 30, 2004, 10:49:20
Job time : 16.4088 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-1

Perfect score: 49

Sequence: 1 KFRHVIDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	55.1	10	3	US-08-836-075A-204
2	27	55.1	12	2	US-08-471-286-1
3	25	51.0	11	4	US-09-418-780A-14
4	25	51.0	11	4	US-09-418-780A-22
5	24	49.0	12	4	US-09-446-787B-91
6	24	49.0	14	3	US-08-909-551-15
7	23	46.9	11	1	US-08-378-761A-68
8	23	46.9	11	1	US-08-485-286-68
9	23	46.9	12	1	US-08-260-582-8
10	23	46.9	12	2	US-08-482-228-98
11	23	46.9	12	3	US-08-482-528-98
12	23	46.9	12	5	PCR-US95-05471-8
13	23	46.9	13	2	US-08-482-228-99
14	23	46.9	13	3	US-08-482-528-99
15	23	46.9	13	3	US-08-974-549A-85
16	23	46.9	13	4	US-08-912-951-85
17	23	46.9	13	4	US-09-402-181B-85
18	23	46.9	13	4	US-09-721-456-85
19	22	44.9	9	2	US-08-646-981-13
20	22	44.9	10	3	US-09-105-839D-72
21	22	44.9	10	4	US-09-344-040C-114
22	22	44.9	10	4	US-09-833-039A-114
23	22	44.9	12	1	US-07-778-231B-29
24	22	44.9	12	1	US-07-963-321-29
25	22	44.9	12	1	US-08-290-641-29
26	22	44.9	12	1	US-08-548-540-29
27	22	44.9	12	4	US-09-446-787B-67

28	22	44.9	12	5	PCT-US96-09809-29	Sequence 29, Appl
29	21	42.9	8	1	US-08-256-236-7	Sequence 7, Appl
30	21	42.9	8	1	US-08-256-236-8	Sequence 8, Appl
31	21	42.9	8	5	PCT-US93-00228-7	Sequence 7, Appl
32	21	42.9	8	5	PCT-US93-00228-8	Sequence 8, Appl
33	21	42.9	9	3	US-08-159-339A-1002	Sequence 1002, Ap
34	21	42.9	9	4	US-09-601-729-252	Sequence 252, Ap
35	21	42.9	10	1	US-08-256-236-10	Sequence 10, Appl
36	21	42.9	10	1	US-08-397-633A-93	Sequence 93, Appl
37	21	42.9	10	2	US-08-556-597-122	Sequence 122, Appl
38	21	42.9	10	3	US-08-836-075A-205	Sequence 205, Appl
39	21	42.9	10	5	PCT-US93-00228-10	Sequence 10, Appl
40	21	42.9	11	1	US-08-503-062-8	Sequence 8, Appl
41	21	42.9	11	5	PCT-US96-11495-8	Sequence 8, Appl
42	21	42.9	12	2	US-08-873-563A-31	Sequence 31, Appl
43	21	42.9	12	2	US-08-873-559-31	Sequence 31, Appl
44	21	42.9	12	3	US-08-993-235-11	Sequence 11, Appl
45	21	42.9	12	4	US-09-226-666-7	Sequence 7, Appl

ALIGNMENTS

```
RESULT 1
US-08-836-075A-204
Sequence 204, Application US/08836075A
Patent No. 6180768
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
TITLE OF INVENTION: SEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-075A-204
Query Match 55.1%; Score 27; DB 3; Length 10;
Best local Similarity 50.0%; Pred. No. 47;
Matches 4; Conservative 3; Mismatches 1; Gaps 0;
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QY 1 KHRVTKD 8
|:|:|:
Db 3 KHRVTKD 10

RESULT 2

US-08-471-286-1
; Sequence 1, Application US/08471286
; Patent No. 5866688
; GENERAL INFORMATION:
; APPLICANT: Kim, Hyesook
; APPLICANT: Charnock, Jonathan
; APPLICANT: Putt, David A.
; APPLICANT: Kim, Edward Y.
; TITLE OF INVENTION: PRODUCTION OF ANTI-PEPTIDE ANTIBODIES
; TITLE OF INVENTION: AGAINST CYTOCHROME P450
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Reising, Ethington, Barnard & Perry
; STREET: P.O. Box 4390
; CITY: Troy
; STATE: Michigan
; COUNTRY: US
; ZIP: 48069-4390
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,286
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kohn, Kenneth I.
; REGISTRATION NUMBER: 30,955
; REFERENCE/DOCKET NUMBER: P-301 (Oxford)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (810) 689-3500
; TELEFAX: (810) 689-4071
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-286-1

Query Match 55.1%; Score 27; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRYVKD 8
|:|:|:
Db 7 HRYVKD 12

RESULT 3

US-09-418-780A-14
; Sequence 14, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-780A-14

Query Match 51.0%; Score 25; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIX 7
|:|:|:
Db 1 YHKIIR 6

RESULT 4

US-09-418-780A-22
; Sequence 22, Application US/09418780A
; Patent No. 6504009
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/09/418,780A
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-418-780A-22

Query Match 51.0%; Score 25; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRVIX 7
|:|:|:
Db 1 YHKIIR 6

RESULT 5

US-09-446-787B-91
; Sequence 91, Application US/09446787B
; Patent No. 6541198
; GENERAL INFORMATION:
; APPLICANT: Akzo No. 6541198el N.V.
; APPLICANT: Paulij, Wilhemina P.
; APPLICANT: Van Kessel-Koens, Marjolijn J.
; TITLE OF INVENTION: Antibodies and other binding molecules specific for hepatitis B vi
; TITLE OF INVENTION: antigens
; FILE REFERENCE: 9310-19
; CURRENT APPLICATION NUMBER: US/09/446,787B
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.01
; SEQ ID NO 91
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-09-446-787B-91

Query Match 49.0%; Score 24; DB 4; Length 12;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIXD 8

Db 4 FHQALQD 10

RESULT 6

US-08-909-551-15

Sequence 15, Application US/08903551

Patent No. 6261569

GENERAL INFORMATION:

APPLICANT: COMIS, ALFIO

APPLICANT: FISCHER, PETER

APPLICANT: TYLER, MARGARET I

TITLE OF INVENTION: Retro-, Inverso-, and Retro-Inverso

TITLE OF INVENTION: Synthetic Peptide Analogues

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr., P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: United States of America

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vers. #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/909,551

FILING DATE: 12-AUG-1997

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/387,932

FILING DATE: 27-FEB-1995

APPLICATION NUMBER: PCT/AU93/00441

FILING DATE: 27-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU 4374

FILING DATE: 27-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: GH0205A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200

TELEFAX: 215-540-5818

TELEX:

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: internal

ORIGINAL SOURCE:

ORGANISM: Hepatitis B virus

FEATURE:

NAME/KEY: Region

LOCATION: 1..14

OTHER INFORMATION: /label= A

OTHER INFORMATION: /note= "THIS PEPTIDE CORRESPONDS TO RESIDUES

PUBLICATION INFORMATION: 127-140 OF THE PRE S PROTEIN OF HBV."

DOCUMENT NUMBER: AU P4374

FILING DATE: 27-AUG-1992

US-08-909-551-15

Query Match 49.0%; Score 24; DB 3; Length 14;

Best Local Similarity 42.9%; Pred. No. 2.4e+02;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FHVXKD 8
Db 1 FHQTLQD 7

RESULT 7

US-08-378-761A-68

Sequence 68, Application US/08378761A

Patent No. 5635384

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESSES:

ADDRESSEE: ANDREA T. BORUCKI

STREET: 9330 ZIONSVILLE ROAD

CITY: INDIANAPOLIS

STATE: IN

COUNTRY: US

ZIP: 46268

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/378,761A

FILING DATE: 26-JAN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BORUCKI, ANDREA T.

REGISTRATION NUMBER: 33651

REFERENCE/DOCKET NUMBER: 38272B

TELECOMMUNICATION INFORMATION:

TELEPHONE: (317) 337-4846

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-378-761A-68

Query Match 46.9%; Score 23; DB 1; Length 11;

Best Local Similarity 80.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RVVXKD 8
Db 6 RVVXKD 10

RESULT 8

US-08-485-286-68

Sequence 68, Application US/08485286

Patent No. 5646026

Patent No. 5646026 5646119

GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

CORRESPONDENCE ADDRESSES:

ADDRESSEE: ANDREA T. BORUCKI

STREET: 9330 ZIONSVILLE ROAD

CITY: INDIANAPOLIS
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,286
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38272B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-485-286-68

Query Match 46.9%; Score 23; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RVYKD 8
Db 6 RVYKD 10

RESULT 9
US-08-260-582-8
Sequence 8, Application US/08260582
Patent No. 5635182
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
APPLICANT: Lu, Zhijian
TITLE OF INVENTION: METHOD OF DETECTING LIGAND
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,582
FILING DATE: 16-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-260-582-8

Query Match 46.9%; Score 23; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFRVYKD 6
Db 3 KFRVYKD 8

RESULT 10
US-08-482-228-98
Sequence 98, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Teeng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: SELECTIVE AND POSITIVE/NEGATIVE CELL
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-482-228-98

Query Match 46.9%; Score 23; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFRVYKD 8
Db 5 EFLRCIKD 12

RESULT 11

US-08-482-528-98
Sequence 98, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-482-528-98

Query Match 46.9%; Score 23; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFRVYKD 8
Db 5 EFLRCIKD 12

RESULT 12
PCT-US93-05471-8
Sequence 8, Application PC/TUS9505471
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
NUMBER OF SEQUENCES: 76
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05471
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
PCT-US95-05471-8
Query Match 46.9%; Score 23; DB 5; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFRVYI 6
Db 3 KFRYMI 8

RESULT 13
US-08-482-228-99
Sequence 99, Application US/08482228
Patent No. 5968753
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,228
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-482-228-99

Query Match 46.9%; Score 23; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFRVYKD 8
Db 6 EFLRCIKD 13

RESULT 14
US-08-482-528-99
Sequence 99, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.

APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deane, Robert J.
TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630CIP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-482-528-99

Query Match 46.9%; Score 23; DB 3; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFRVYIKD 8
DB 6 EFLRCKD 13

RESULT 15
US-08-974-549A-85
Sequence 85, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linsner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..13
OTHER INFORMATION: motif C peptide from Schizosaccharomyces
OTHER INFORMATION: pombe TRT
US-08-974-549A-85

Query Match 46.9%; Score 23; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RVYKDF 9
DB 4 RVYKDF 9

RESULT 16
US-08-912-951-85
Sequence 85, Application US/08912951
Patent No. 6475789
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Linsner, Joachim
APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Hayley, Calvin H.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND
THERAPEUTIC METHODS
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/912,951
FILING DATE: 14-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015399-002600US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..13
OTHER INFORMATION: /note="telomerase RT palm, primer grip
OTHER INFORMATION: motif C peptide from Schizosaccharomyces
OTHER INFORMATION: pombe TRT"
US-08-912-951-85

Query Match 46.9%; Score 23; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
4 RVKDF 9
4 RVDVF 9
Db

RESULT 17
US-09-402-181B-85
Sequence 85, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Hayley, Calvin H.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ausubius, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..13
OTHER INFORMATION: /note="telomerase RT palm, primer grip
OTHER INFORMATION: motif C peptide from Schizosaccharomyces
OTHER INFORMATION: pombe TRT"
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-09-402-181B-85

Query Match 46.9%; Score 23; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 18

US-09-721-456-85
Sequence 85, Application US/09721456
Patent No. 6617110

GENERAL INFORMATION:

APPLICANT: Cecchi, Thomas R.
Insgner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-Nov. 6617110-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-Nov-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-Oct-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-Apr-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-Apr-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-May-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-May-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-Aug-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-Oct-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-Oct-1997

ATTORNEY/AGENT INFORMATION:

NAME: Apple, Randolph Red
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..13
OTHER INFORMATION: /note="telomerase RT palm, primer grip
motif C peptide from Schizosaccharomyces
pombe TR1"
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-09-721-456-85

Query Match 46.9%; Score 23; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RVKDF 9
DB 4 RYVDF 9

RESULT 19

US-08-646-981-13
Sequence 13, Application US/08646981
Patent No. 5852183

GENERAL INFORMATION:

APPLICANT: MAEDA, HIROAKI
APPLICANT: EDA, YASUYUKI
APPLICANT: KIMACHI, KAZUHIKO
APPLICANT: ONO, YOICHI
APPLICANT: TOKIYOSHI, SACHIO
TITLE OF INVENTION: DOG-MOUSE HETEROHYBRIDOMA AND GENE
TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,981
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1488-106
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-646-981-13

Query Match 44.9%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1

QY 5 VIKDF 9
DB 2 LKDF 6

RESULT 20
US-09-105-839D-72
; Sequence 72, Application US/09105839D
; Patent No. 6287756
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Chen, Yao-Tseeng
; APPLICANT: Sahin, Ugur
; APPLICANT: Gure, Ali
; APPLICANT: Old, Lloyd J
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Method for Determining Presence of Cancer in A Sample By Determin
; FILE REFERENCE: LUD 5556
; CURRENT FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-105-839D-72

Query Match
Best Local Similarity 44.9%; Score 22; DB 3; Length 10;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFHRYI 6
: ||:|
Db 5 RLHRII 10

RESULT 21
US-09-344-040C-114
; Sequence 114, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In A Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344, 040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 114
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-114

Query Match
Best Local Similarity 44.9%; Score 22; DB 4; Length 10;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFHRYI 6
: ||:|
Db 5 RLHRII 10

RESULT 22
US-09-833-039A-114
; Sequence 114, Application US/09833039A

Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 114
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-114

Query Match
Best Local Similarity 44.9%; Score 22; DB 4; Length 10;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFHRYI 6
: ||:|
Db 5 RLHRII 10

RESULT 23
US-07-778-233B-29
; Sequence 29, Application US/0778233B
; Patent No. 5270170
; GENERAL INFORMATION:
; APPLICANT: Schatz, Peter J.
; APPLICANT: Cull, William G.
; APPLICANT: Miller, Jeff F.
; TITLE OF INVENTION: Peptide Library and Screening Method
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/778,233B
; FILING DATE: 19911016
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-50
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:

CLONE: 26 4 0.8
US-07-778-2338-29

Query Match 44.9%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
|||:
Db 6 HRVIR 10

RESULT 24
US-07-963-321-29

Sequence 29, Application US/07963321

Patent No. 5338665

GENERAL INFORMATION:

APPLICANT: Schatz, Peter J.

APPLICANT: Cull, Millaard G.

APPLICANT: Miller, Jeff F.

APPLICANT: Stemmer, William P.C.

TITLE OF INVENTION: Peptide Library and Screening Method

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/963.321

FILING DATE: 19921015

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/778.223

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11509-50-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2422

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: AMINO ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: 26 4 0.8

US-07-963-321-29

Query Match 44.9%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
|||:
Db 6 HRVIR 10

RESULT 25
US-08-290-641-29

Sequence 29, Application US/08290641

Patent No. 5498530

GENERAL INFORMATION:

APPLICANT: Schatz, Peter J.

APPLICANT: Cull, Millaard G.

APPLICANT: Miller, Jeff F.

APPLICANT: Stemmer, William P.C.

TITLE OF INVENTION: Peptide Library and Screening Method

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/290.641

FILING DATE: 15-AUG-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/963.321

FILING DATE: 15-OCT-1992

APPLICATION NUMBER: US 07/778.223

FILING DATE: 16-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11509-50-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2422

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

CLONE: 26 4 0.8

US-08-290-641-29

Query Match 44.9%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
|||:
Db 6 HRVIR 10

RESULT 26
US-08-548-540-29

Sequence 29, Application US/08548540

Patent No. 5733731

GENERAL INFORMATION:

APPLICANT: Schatz, Peter J.

APPLICANT: Cull, Millaard G.

APPLICANT: Miller, Jeff F.

APPLICANT: Stemmer, William P.C.

TITLE OF INVENTION: Peptide Library and Screening Method

NUMBER OF SEQUENCES: 162

CORRESPONDENCE ADDRESS:

ADDRESSEE: William M. Smith

STREET: One Market Plaza, Stewart Tower, Suite 2000

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/548,540
FILING DATE: 26-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528J-001240US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 26 4 0.8
US-08-548-540-29

Query Match 44.9%; Score 22; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
DB 6 HRVIR 10

RESULT 27
US-09-446-787B-67
Sequence 67, Application US/09446787B
Patent No. 6541198
GENERAL INFORMATION:
APPLICANT: Akzo No. 6541198a1 N.V.
APPLICANT: Paulij, Wilhemina P.
APPLICANT: Van Kessel-Koenen, Marijolin J.
TITLE OF INVENTION: Antibodies and other binding molecules specific for hepatitis B v
FILE REFERENCE: 9310-19
CURRENT APPLICATION NUMBER: US/09/446,787B
CURRENT FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.1
SEQ ID NO 67
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic polypeptide
US-09-446-787B-67

Query Match 44.9%; Score 22; DB 4; Length 12;
Best Local Similarity 42.9%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 HRVIR 8
DB 4 HQALAD 10

RESULT 28
PCT-US96-09809-29
Sequence 29, Application PC/TUS9609809
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
APPLICANT: Call, Willard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, William P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09809
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,540
FILING DATE: 26-OCT-1995
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 16528J-001240US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 26 4 0.8
PCT-US96-09809-29

Query Match 44.9%; Score 22; DB 5; Length 12;
Best Local Similarity 60.0%; Pred. No. 4.8e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
DB 6 HRVIR 10

RESULT 29
US-08-256-236-7
Sequence 7, Application US/08256236
Patent No. 5563121
GENERAL INFORMATION:
APPLICANT: Janda, Kim
APPLICANT: Wirsching, Peter
APPLICANT: Ikeda, Shoji
TITLE OF INVENTION: Peptide Linkage Unit

NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 5563121th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,236
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00228
FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/819,356
FILING DATE: 09-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Donald G. Lewis
REGISTRATION NUMBER: 28,636
REFERENCE/DOCKET NUMBER: TSR1279.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-619-554-2937
TELEFAX: 1-619-554-6312
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="Xaa is Leu whose carbonyl
OTHER INFORMATION: group is replaced by PO(OH)CH2"
US-08-256-236-7

Query Match 42.9%; Score 21; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FHVI 6
Db 3 FHVI 7

RESULT 30
US-08-256-236-8
Sequence 8, Application US/08256236
Patent No. 5563121
GENERAL INFORMATION:
APPLICANT: Janda, Kim
APPLICANT: Wirsching, Peter
APPLICANT: Ikeda, Shoji
TITLE OF INVENTION: Peptide Linkage Unit
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 5563121th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,236
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00228
FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/819,356
FILING DATE: 09-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Donald G. Lewis
REGISTRATION NUMBER: 28,636
REFERENCE/DOCKET NUMBER: TSR1279.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-619-554-2937
TELEFAX: 1-619-554-6312
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="Xaa is N-C-Boc-His"
OTHER INFORMATION: group is replaced by PO(OH)CH2"
US-08-256-236-8

Query Match 42.9%; Score 21; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FHVI 6
Db 3 FHVI 7

RESULT 31
PCT-US93-00228-7
Sequence 7, Application PC/TUS9300228
GENERAL INFORMATION:
APPLICANT: Janda, Kim
APPLICANT: Wirsching, Peter
APPLICANT: Ikeda, Shoji
TITLE OF INVENTION: Peptide Linkage Unit
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: The Scripps Research Institute,
Office of Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00228
FILING DATE: 19930111
CLASSIFICATION:

Prior Application Data:
Application Number: US 07/819,356
Filing Date: 09-Jan-92
Attorney/Agent Information:
Name: Lewis, Donald G.
Registration Number: 28,636
Reference/Docket Number: tsr1279.0(PC)
Telecommunication Information:
Telephone: 1-619-5542937
Telefax: 1-619-554-6312
Information for SEQ ID NO: 7:
Sequence Characteristics:
Length: 8 amino acids
Type: AMINO ACID
Strandedness: single
Topology: linear
Molecule Type: peptide
Feature:
Name/Key: Modified-site
Location: 5
Other Information: /label=Xaa
Other Information: /note="Xaa is Leu whose carbonyl group is
OTHER INFORMATION: replaced by PO(OH)CH2"
PCT-US93-00228-7

Query Match 42.9%; Score 21; DB 5; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHXYI 6
DB 3 FHXYI 7

RESULT 32
PCT-US93-00228-8
Sequence 8, Application PC/TUS9300228
GENERAL INFORMATION:
APPLICANT: Janda, Kim
APPLICANT: Wirsching, Peter
APPLICANT: Ikeda, Shoji
TITLE OF INVENTION: Peptide Linkage Unit
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute,
ADDRESS: Office of Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00228
FILING DATE: 19930111
CLASSIFICATION:
Prior Application Data:
Application Number: US 07/819,356
Filing Date: 09-Jan-92
Attorney/Agent Information:
Name: Lewis, Donald G.
Registration Number: 28,636
Reference/Docket Number: tsr1279.0(PC)
Telecommunication Information:
Telephone: 1-619-5542937
Telefax: 1-619-554-6312
Information for SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids

TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
Name/Key: Modified-site
Location: 1
Other Information: /label=Xaa
Other Information: /note="Xaa is N-t-Boc-His"
Feature:
Name/Key: Modified-site
Location: 5
Other Information: /label=Xaa
Other Information: /note="Xaa is Leu whose carbonyl group is
OTHER INFORMATION: replaced by PO(OH)CH2"
PCT-US93-00228-8

Query Match 42.9%; Score 21; DB 5; Length 8;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHXYI 6
DB 3 FHXYI 7

RESULT 33
US-08-159-339A-1002
Sequence 1002, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard W.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
Prior Application Data:
Application Number: US 07/926,666
Filing Date: 07-AUG-1992
Application Number: US 08/027,746
Filing Date: 05-MAR-1993
Application Number: US 08/103,396
Filing Date: 06-AUG-1993
Attorney/Agent Information:
Name: Weber, Ellen Lauver
Registration Number: 32,762
Reference/Docket Number: 018623-005030US
Telecommunication Information:
Telephone: (415) 576-0200
Telefax: (415) 576-0300
TELEX:
Information for SEQ ID NO: 1002:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
Type: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-1002

Query Match 42.9% Score 21; DB 3; Length 9;
Best Local Similarity 44.4% Pred. No. 3e+05;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 FHRVIXDF 9
DB 1 FRRRTETDF 9

RESULT 34
US-09-601-729-252
Sequence 252, Application US/09601729
Patent No. 6683052
GENERAL INFORMATION:
APPLICANT: THIAM, KADER
APPLICANT: AURIAUT, CLAUDE
APPLICANT: GRAS-MASSE, HELENE
APPLICANT: LOING, ESTELLE
APPLICANT: VERWAERDE, CLAUDE
APPLICANT: GUILLET, JEAN GERARD
TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
FILE REFERENCE: US-97-AU-IN
CURRENT APPLICATION NUMBER: US/09/601.729
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/FR99/00259
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 98 01439
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 252
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-601-729-252

Query Match 42.9% Score 21; DB 4; Length 9;
Best Local Similarity 42.9% Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FHRVIXD 8
DB 2 FHRVARE 8

RESULT 35
US-08-256-236-10
Sequence 10, Application US/08256236
Patent No. 5563121
GENERAL INFORMATION:
APPLICANT: Janda, Kim
APPLICANT: Wirsching, Peter
APPLICANT: Ikeda, Shoji
TITLE OF INVENTION: Peptide Linkage Unit
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute
STREET: 10666 No. 5563121th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256.236
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00228
FILING DATE: 11-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/819,356
FILING DATE: 09-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Donald G. Lewis
REGISTRATION NUMBER: 28,636
REFERENCE/DOCKET NUMBER: TSI1279.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-619-554-2937
TELEFAX: 1-619-554-6312
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa is Ieu whose carbonyl
OTHER INFORMATION: group is replaced by PO(OH)CH2"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa is N-epsilon-L-BOC-Lys
OTHER INFORMATION: methyl ester"
US-08-256-236-10

Query Match 42.9% Score 21; DB 1; Length 10;
Best Local Similarity 80.0% Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVI 6
DB 4 FHRVI 8

RESULT 36
US-08-397-633A-93
Sequence 93, Application US/08397633A
Patent No. 573577
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
NUMBER OF SEQUENCES: 105
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/397.633A
FILING DATE:

CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-397-633A-93

Query Match 42.9%; Score 21; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVI 6
Db 6 HRVI 9

RESULT 37
US-08-556-597-122
Sequence 122, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-122

Query Match 42.9%; Score 21; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRVIR 7
Db 3 WRRPIK 8

RESULT 38
US-08-836-075A-205
Sequence 205, Application US/08836075A
Patent No. 6180768
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
APPLICANT: STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,075A
FILING DATE: 21 Apr 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP95/04155
FILING DATE: 23 Oct 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-836-075A-205

Query Match 42.9%; Score 21; DB 3; Length 10;
Best Local Similarity 25.0%; Pred. No. 6.2e+02;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFRVIRKD 8
Db 3 RMHQVVOE 10

RESULT 39
PCT-US93-00228-10
Sequence 10, Application PC/TUS9300228
GENERAL INFORMATION:
APPLICANT: Janda, Kim
APPLICANT: Wirsching, Peter
APPLICANT: Ikeda, Shoji
TITLE OF INVENTION: Peptide Linkage Unit
NUMBER OF SEQUENCES: 32

```

CORRESPONDENCE ADDRESS:
ADDRESSER: The Scripps Research Institute,
ADDRESSEE: Office of Patent Counsel
STREET: 10666 North Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00228
FILING DATE: 19930111
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/819,356
FILING DATE: 09-Jan-92
ATTORNEY/AGENT INFORMATION:
NAME: Lewis, Donald G.
REGISTRATION NUMBER: 28,636
REFERENCE/DOCKET NUMBER: tefi279.0(PC)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-619-5542937
TELEFAX: 1-619-554-6312
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa is Leu whose carbonyl group is
FEATURE:
NAME/KEY: Modified-site
LOCATION: 10
OTHER INFORMATION: /label= Xaa
OTHER INFORMATION: /note= "Xaa is N-epsilon-L-tyrosine methyl ester"
PCT-US93-00228-10
Query Match 42.9%; Score 21; DB 5; Length 10;
Best Local Similarity 80.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CY 2 FHRVI 6
DB 4 FHXVI 8
RESULT 40
US-08-503-062-8
Sequence 8, Application US/08503062
GENERAL INFORMATION:
APPLICANT: Denis, Gerald V.
APPLICANT: Green, Michael R.
TITLE OF INVENTION: NUCLEAR LOCALIZED TRANSCRIPTION FACTOR
TITLE OF INVENTION: KINASES AND DIAGNOSTIC ASSAYS RELATED THERETO
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/503,062
FILING DATE: 10-JUL-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 04020/080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-503-062-8
Query Match 42.9%; Score 21; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
CY 2 FHRVIK 7
DB 1 YHDIK 6
RESULT 41
PCT-US96-11495-8
Sequence 8, Application PC/TUS9611495
GENERAL INFORMATION:
APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL CENTER
TITLE OF INVENTION: NUCLEAR LOCALIZED TRANSCRIPTION FACTOR
TITLE OF INVENTION: KINASES AND DIAGNOSTIC ASSAYS RELATED THERETO
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/11495
FILING DATE: 03-JUL-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/503,062
FILING DATE: 10-JUL-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-11495-8

Query Match 42.9%; Score 21; DB 5; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 2 FHRVYK 7
|:|
Db 1 YHDIK 6

RESULT 42
US-08-973-563A-31
Sequence 31, Application US/08973563A
Patent No. 5885965

GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.

APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter

APPLICANT: Roberts, F. D.

APPLICANT: Friden, Philip M.

TITLE OF INVENTION: Anti-Fungal D-Amino Acid Histatin-Based

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,563A

FILING DATE: 07-JUN-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,273

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: PER95-02A2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-9540

TELEFAX: 781-861-9540

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:
NAME/KEY: Region

LOCATION/KEY: 1..12

OTHER INFORMATION: /note="At least one amino acid

US-08-973-563A-31

Query Match 42.9%; Score 21; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPHR 4
|:|
Db 6 KYHR 9

RESULT 43
US-08-973-559-31
Sequence 31, Application US/08973559
Patent No. 5912230

GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.

APPLICANT: Xu, Tao

APPLICANT: Roberts, F. D.

APPLICANT: Spacciapoli, Peter

APPLICANT: Friden, Philip M.

TITLE OF INVENTION: Anti-Fungal and Anti-Bacterial

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:
ADDRESS: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Millitia Drive

CITY: Lexington

STATE: MA

COUNTRY: US

ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,559

FILING DATE: 07-JUN-1996

CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,888

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.

REGISTRATION NUMBER: 22,592

REFERENCE/DOCKET NUMBER: PER95-01A2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 781-861-9540

TELEFAX: 781-861-9540

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-973-559-31

Query Match 42.9%; Score 21; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KPHR 4
|:|
Db 6 KYHR 9

RESULT 44
US-08-993-235-11

Sequence 11, Application US/08993235
Patent No. 6084064

GENERAL INFORMATION:
APPLICANT: Oppenheim, Frank G.

APPLICANT: Xu, Tao

APPLICANT: Spacciapoli, Peter

APPLICANT: Roberts, F. DONALD

TITLE OF INVENTION: ANTIFUNGAL AND ANTIBACTERIAL PEPTIDES

FILE REFERENCE: 50032/002001

;; CURRENT APPLICATION NUMBER: US/08/993,235
;; CURRENT FILING DATE: 1997-12-18
;; NUMBER OF SEQ ID NOS: 13
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 11
;; LENGTH: 12
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-08-993-235-11

Query Match 42.9%; Score 21; DB 3; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHR 4
|:|
Db 6 KYHR 9

RESULT 45
US-09-226-666-7
; Sequence 7, Application US/09226666A
; Parent No. 6528488
; GENERAL INFORMATION:
; APPLICANT: Spacciapoli, Peter
; APPLICANT: Rothstein, David M.
; APPLICANT: Fridgen, Phillip M.
; TITLE OF INVENTION: METHOD FOR TREATING CYSTIC FIBROSIS
; FILE REFERENCE: 50032/007001
; CURRENT APPLICATION NUMBER: US/09/226,666A
; CURRENT FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Derived from Homo sapiens
US-09-226-666-7

Query Match 42.9%; Score 21; DB 4; Length 12;
Best Local Similarity 75.0%; Pred. No. 7.4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KHR 4
|:|
Db 6 KYHR 9

Search completed: August 30, 2004, 10:57:09
Job time : 5.55743 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 2.70608 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: us-09-720-469a-1

Perfect score: 49

Sequence: 1 KFHRTV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	44.9	12	2	PC4377
2	19	38.8	8	2	S65381
3	19	38.8	13	2	A61361
4	18	36.7	12	2	S10624
5	17	34.7	14	2	E61308
6	16	32.7	9	2	D57444
7	16	32.7	10	1	EC104M
8	16	32.7	10	2	B93108
9	16	32.7	10	2	S36848
10	16	32.7	10	2	PC4374
11	16	32.7	12	2	S01222
12	16	32.7	14	2	A01250
13	16	32.7	14	2	PT0254
14	16	32.7	14	2	AF0296
15	15	30.6	11	4	I52708
16	15	30.6	12	2	PO0730
17	15	30.6	12	2	PT0228
18	15	30.6	14	2	A28018
19	14	28.6	8	2	USC316
20	14	28.6	8	2	S66296
21	14	28.6	9	2	E28854
22	14	28.6	9	2	US0302
23	14	28.6	9	2	A60320
24	14	28.6	9	2	A44787
25	14	28.6	9	2	S78420
26	14	28.6	10	2	B46453
27	14	28.6	10	2	I40032
28	14	28.6	10	2	S65432
29	14	28.6	10	2	B56899

30	14	28.6	10	2	A90345	angiotensin precu
31	14	28.6	10	2	S65387	cytochrome-c oxida
32	14	28.6	11	2	G42762	proteasome endopep
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34	14	28.6	11	2	I54193	Rhesus blood group
35	14	28.6	11	2	PN0042	stachin - mouse (
36	14	28.6	11	2	PH1376	T antigen variant
37	14	28.6	12	2	S09082	proteasome chain 1
38	14	28.6	13	2	G44644	neurotoxin-associ
39	14	28.6	13	2	S36887	ribosomal protein
40	14	28.6	13	2	PN0168	phosphopyruvate hy
41	14	28.6	13	2	H85575	hypothetical prote
42	14	28.6	14	2	PC0152	18k iron-sulfur pr
43	14	28.6	14	2	A61308	hemocyanin chain 2
44	14	28.6	14	2	S29486	GTP-binding protei
45	14	28.6	14	2	G33160	H+-transporting tw

ALIGNMENTS

RESULT 1
PC4377
telomeric and tetraplex DNA binding protein qTBP42 VIII - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C/Accession: PC4377
R/Saig, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A/Title: telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A/Reference number: PC4377; PMID:97445086; PMID:9299414
A/Accession: PC4377
A/Molecule type: protein
A/Residues: 112 <SAR>
C/Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 44.9%; Score 22; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.7e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFHRTV 5
DB 3 KFHRTV 7

RESULT 2
S65381
cytochrome-c oxidase (EC 1.9.3.1) chain VIB, hepatic - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C/Accession: S65381
R/Saenger, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A/Title: cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A/Reference number: S65372; PMID:95324529; PMID:7601105
A/Accession: S65381
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <SCH>
C/Keywords: oxidoreductase

Query Match 38.8%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHR 4
DB 6 FHR 8

RESULT 3
A61361
bradykinin-like peptide - Bombina orientalis

C:Species: Bombina orientalis
 C>Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
 C/Accession: A61361
 R:Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaiharu, N.; Yanaiharu, C.; Hashimoto, T.; Sak
 Chem. Pharm. Bull. 21, 1368-1391, 1973
 A:Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger an
 A:Reference number: A61361; MUID:73256922; PMID:4732297
 A:Accession: A61361
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <YAS>
 C:Superfamily: unassigned animal peptides
 C:Keywords: skin

Query Match 38.8%; Score 19; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KFH 3
 |||
 Db 11 KFH 13

RESULT 4
 S10624
 lipovitelin - African clawed frog
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C/Accession: S10624
 R:Wallace, R.A.; Hoch, K.L.; Carnevali, O.
 J. Moll. Biol. 213, 407-409, 1990
 A:Title: Placement of small lipovitelin subunits within the vitellogenin precursor in X
 A:Reference number: S10624; MUID:90278951; PMID:2352275
 A:Accession: S10624
 A:Molecule type: protein
 A:Residues: 1-12 <WAL>

Query Match 36.7%; Score 18; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 2.3e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 KFHVIK 7
 |||
 Db 1 KFORPYK 7

RESULT 5
 E61308
 hemocyanin chain 3B - Sahara scorpion (fragment)
 C:Species: Androctonus australis (Sahara scorpion)
 C>Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C/Accession: E61308
 R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
 FEBS Lett. 106, 289-291, 1979
 A:Title: Structural characterization of seven different subunits in Androctonus australis
 A:Reference number: A61308; MUID:80047238; PMID:499512
 A:Accession: E61308
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <JOL>

Query Match 34.7%; Score 17; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RVIKDF 9
 |||
 Db 8 RILKLF 13

RESULT 6
 D57444
 neuropeptide Grb-AST B4 - two-spotted cricket

C:Species: Gryllus bimaculatus (two-spotted cricket)
 C>Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
 C/Accession: D57444
 R:Lorenz, M.W.; Keilner, R.; Hoffmann, K.H.
 J. Biol. Chem. 270, 21103-21108, 1995
 A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cric
 A:Reference number: A57444; MUID:95403341; PMID:7673141
 A:Accession: D57444
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <LOR>

Query Match 32.7%; Score 16; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KFH 3
 |||
 Db 4 RFH 6

RESULT 7
 ECL04M
 tachykinin IV - migratory locust
 N:Alternate names: locusttachykinin IV
 C:Species: Locusta migratoria (migratory locust)
 C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 08-Dec-1995
 C/Accession: B60073
 R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Kochaneky, J.P.; Nachman, R.J.; De Loof, A.
 Regul. Pept. 31, 199-212, 1990
 A:Title: Locusttachykinin III and IV: two additional insect neuropeptides with homology
 A:Reference number: A60073; MUID:91219696; PMID:2132575
 A:Accession: B60073
 A:Molecule type: protein
 A:Residues: 1-10 <SCH>
 C:Superfamily: tachykinin
 C:Keywords: amidated carboxyl end; neuropeptide; tachykinin
 F:10/Modified site: amidated carboxyl end (Arg) #status experimental

Query Match 32.7%; Score 16; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FHRV 5
 |||
 Db 6 FHGV 9

RESULT 8
 B39308
 glycine reductase (EC 1.4.99.-) sulphydryl protein C, beta chain - Clostridium sticklandii
 C:Species: Clostridium sticklandii
 C>Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
 C/Accession: B39308
 R:Stadtman, T.C.; Davis, J.N.
 J. Biol. Chem. 266, 22147-22153, 1991
 A:Title: Glycine reductase protein C. Properties and characterization of its role in the
 A:Reference number: A39308; MUID:92042241; PMID:1939235
 A:Accession: B39308
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <STA>
 C:Function:
 A:Description: glycine reductase complex catalyzes the reductive deamination of glycine t
 C:Keywords: ATP; oxidoreductase

Query Match 32.7%; Score 16; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRVND 8
 |||
 Db 4 NRVND 9

RESULT 9

S36849
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C:Accession: S36849
R:Jacob, J.; Kelsce, G.
Submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A:Reference number: S25024
A:Accession: S36849
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-10 <UAC>
A:Cross-references: EMBL:X67382; NID:G50070; PIDN:CAA47794.1; PID:G51590; PID:G1333861
C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 32.7%; Score 16; DB 2; Length 10;
Best Local Similarity 22.2%; Pred. No. 4.7e+03;
Matches 2; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KFHRYIXDP 9

Db 2 RYRTVVVNF 10

RESULT 10

PC4374
telomeric and tetraplex DNA binding protein qTBP42 IV - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 07-May-1999
C:Accession: PC4374
R:Sariy, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A:Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the C
A:Reference number: PC4374; MUID:97445086; PMID:9299414
A:Accession: PC4374
A:Molecule type: protein
A:Residues: 1-10 <SAR>
C:Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match

Best Local Similarity 32.7%; Score 16; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFHRY 5

Db 6 KEHRL 10

RESULT 11

S01222
translation elongation factor EF-Tu - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C:Accession: S01222
R:Hughes, M.A.; Jones, D.S.
Nucleic Acids Res. 16, 7193, 1988
A:Title: A fragment of the Pseudomonas aeruginosa genome contains five tRNA genes, four
A:Reference number: S01222; MUID:88303352; PMID:3136442
A:Accession: S01222
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-12 <HUG>
A:Cross-references: EMBL:X07950; NID:G45426; PIDN:CAA30775.1; PID:G45427
C:Genetics:
A:Gene: tufr
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolo
C:Keywords: GTP binding; protein biosynthesis

Query Match

32.7%; Score 16; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFHRY 4

Db 5 KFER 8

RESULT 12

A01250
angiotensin precursor - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 15-Sep-2003
C:Accession: A92775; A01250
R:Skoggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A:Reference number: A92775
A:Accession: A92775
A:Molecule type: protein
A:Residues: 1-14 <SKE>
C:Superfamily: Serpin
C:Keywords: blood pressure control; hormone; vasoconstrictor
F,1-10/Product: angiotensin I #status experimental <ANI>
F,1-8/Product: angiotensin II #status experimental <AN2>

Query Match

Best Local Similarity 32.7%; Score 16; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 6.6e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRV 6

Db 8 FHDLV 12

RESULT 13

PT0254
Ig heavy chain CND3 region (clone 2-115A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0254
R:Yamada, M.; Maeseman, R.; Reichard, B.A.; Shane, S.; Caton, A.D.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108357; PMID:1899102
A:Accession: PT0254
A:Molecule type: DNA
A:Residues: 1-14 <YAM>
A:Experimental source: B Lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 32.7%; Score 16; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 6.6e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHR 4

Db 12 YHR 14

RESULT 14

AF0296
phenylalanyl-tRNA synthetase operon leader peptide [imported] - Yersinia pestis (strain
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AF0296
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AF0296
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-14 <KUR>
A:Cross-references: GB:ALU590842; PIDN:CAC91234.1; PID:G15980423; GSEFDB:GN00175
C:Genetics:
A:Gene: pheX

Query Match 32.7%; Score 16; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 6.6e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 HRVIXDF 9
| | | |
DB 2 HTVIFRF 8

RESULT 15

ELAV-like neuronal protein 1, truncated splice form - human
N:Alternate names: Drosophila ELAV(embryonic lethal, abnormal vision)-like 4; Hu antigen
C:Species: Homo sapiens (man)
C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: I52708
R:Seikido, Y.; Badier, S.A.; Carbone, D.P.; Johnson, B.E.; Minna, J.D.
Cancer Res. 54, 4988-4992, 1994
A:Title: Molecular analysis of the Hnd gene encoding a paraneoplastic encephalomyelitis
A:Reference number: I52708; MUID:94345312; PMID:8069866
A:Accession: I52708
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-11 <SEK>
A:Cross-references: GB:S73887; NID:G668242; PIDN:ADD14142.1; PID:G4261842
C:Comment: This abnormal peptide is expressed. For the long splice form, see PIR:I38726.
C:Genetics:
A:Gene: GDB:ELAVL4; HUD; PNEU
A:Cross-references: GDB:141875; OMIM:168360
A:Map position: 1p35-1p36
C:Keywords: alternative splicing

Query Match 30.6%; Score 15; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.1e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 RVIX 7
| | | |
DB 6 RILK 9

RESULT 16

unidentified 5.4/35K protein [imported] - rice (fragment)
PQ0730

C:Species: Oryza sativa (rice)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0730
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library: a data-file of rice proteins separated by two-dimension
A:Reference number: PQ0696
A:Accession: PQ0730
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-12 <KOM>

Query Match 30.6%; Score 15; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 8.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 VIKDF 9
| | | |
DB 3 VVKFF 7

RESULT 17

PT0228

Ig heavy chain CDR3 region (clone 1-112) - human (fragment)

C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0228
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and Jc
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0228
A:Molecule type: DNA
A:Residues: 1-12 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterodimer; immunoglobulin

Query Match 30.6%; Score 15; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 8.9e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RVIKD 8
| | | |
DB 2 RYVRD 6

RESULT 18

A28018
Very late antigen-1 alpha chain - human (fragment)
N:Alternate names: VLA-1 alpha chain
C:Species: Homo sapiens (man)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C:Accession: A28018
R:Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecu
A:Reference number: A94151; MUID:87204112; PMID:3035641
A:Accession: A28018
A:Molecule type: protein
A:Residues: 1-14 <YAK>
C:Keywords: duplication; heterodimer; membrane protein

Query Match 30.6%; Score 15; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FHRVIXD 8
| | | |
DB 1 FNVVDVD 7

RESULT 19

US0316
leucokinin VI - Madeira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: US0316
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A:Title: Isolation, primary structure, and synthesis of leucokinsins V and VI: myotropic f
A:Reference number: US0315
A:Accession: US0316
A:Molecule type: protein
A:Residues: 1-8 <HOL>

C:Comment: Leucokinsins, a family of cephalomyotropic peptides, stimulate contractile acti
C:Keywords: amidated carboxyl end; cephalomyotropic peptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.6%; Score 14; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
| | | |
DB 4 FH 5

RESULT 20

S66296
Na+-transporting ATP synthase (EC 3.6.1.-) chain c - Acetobacterium woodii (fragment)
N:Alternate names: ATPase chain c
C:Species: Acetobacterium woodii
C>Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S66296
R:Reidlinger, U.; Mueller, V.
E:R. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a
A:Reference number: S45648; MUID:94307271; PMID:8033902
A:Accession: S66296
A:Molecule type: protein
A:Residues: 1-8 <R1>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match 28.6%; Score 14; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 IKDF 9
DB 3 ILDF 6

RESULT 21

E28854
Fibrinopeptide B - hamadryas baboon
C:Species: Papio hamadryas (hamadryas baboon)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Aug-2000
C:Accession: E28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: E28854
A:Molecule type: protein
A:Residues: 1-9 <NAK>
C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulf

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FH 3
DB 6 FH 7

RESULT 22

US0302
xenopsin-related peptide 2 - turkey
N:Contains: xenopsin-related peptide 1
C:Species: Melagris gallopavo (common turkey)
C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
C:Accession: US0302
R:Carraway, R.E.; Cochran, D.E.; Mitra, S.P.
Regul. Pept. 22, 303-314, 1988
A:Title: Xenopsin-related peptide generated in avian gastric extracts.
A:Reference number: US0302; MUID:89042995; PMID:2460902
A:Accession: US0302
A:Molecule type: protein
A:Residues: 1-9 <CAR>

C:Comment: The peptides are present within several tissues primarily in large molecular
C:Superfamily: Yeast coatomer complex alpha chain; WD repeat homology
C:Keywords: neuopeptide
F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>
F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 28.6%; Score 14; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FH 3
DB 1 FH 2

RESULT 23

A60320
xenopsin-related peptide 2 - rat
N:Contains: xenopsin-related peptide 1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Aug-2000
C:Accession: A60320
R:Carraway, R.E.; Mitra, S.P.; Muraki, K.
Regul. Pept. 29, 229-239, 1990
A:Title: Isolation and structures of xenopsin-related peptides from rat stomach, liver a
A:Reference number: A60320; MUID:91018491; PMID:2217904
A:Accession: A60320
A:Molecule type: protein
A:Residues: 1-9 <CAR>
A>Note: the authors purified these peptides from pepsin-treated extracts of stomach, liv
C:Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in sequence
C:Superfamily: yeast coatomer complex alpha chain; WD repeat homology
C:Keywords: neuopeptide
F:1-9/Product: xenopsin-related peptide 2 #status experimental <MAT1>
F:2-9/Product: xenopsin-related peptide 1 #status experimental <MAT2>

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FH 3
DB 1 FH 2

RESULT 24

A44787
calliphoramide 10 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: A44787
R:Dive, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; MUID:92196111; PMID:1549595
A:Accession: A44787
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuopeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KDF 9
DB 4 RDF 6

RESULT 25

S78420
ribosomal protein R41, mitochondrial [validated] - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: S78420
R:Goldschmidt-Reisin, S.; Grack, H.R.
submitted to the Protein Sequence Database, February 1998
A:Reference number: S78411

A:Accession: S78420
A:Molecule type: protein
A:Residues: 1-9 <SOL>
A>Note: the protein is designated as mitochondrial ribosomal protein L41
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 28.6%; Score 14; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRV 5
||
5 HRL 7

RESULT 26

B46453
e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)
N:Alternate names: HBe antigen precursor
N:Contains: e antigen
C:Species: hepatitis B virus, HBV
A:Variety: subtype adr
C>Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997
C:Accession: B46453
R:Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda, J. Immunol. 147, 3156-3160, 1991
A:Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepa
A:Reference number: A46453; MUID:92013147; PMID:1717588
A:Accession: B46453
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <TRX>
A:Experimental source: subtype adr
A>Note: sequence extracted from NCBI backbone (NCBIP:60243)
F:1-10/Domain: signal sequence (fragment) #status predicted <Sig>

Query Match 28.6%; Score 14; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
||
4 FH 5

RESULT 27

I40032
tPB protein - Bacillus amyloliquefaciens (fragment)
C:Species: Bacillus amyloliquefaciens
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 15-Oct-1999
C:Accession: I40032
R:Yoshimura, K.; Demura, J.; Seki, T.; Oshima, Y.
J. Bacteriol. 159, 905-912, 1984
A:Title: Construction of a promoter-probe vector for Bacillus subtilis host by using the
A:Reference number: I40032; MUID:85006754; PMID:6090398
A:Accession: I40032
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-10 <RBS>
A:Cross-references: GB:K02661; NID:G143775; PID:AB05353.1; PID:G143776

Query Match 28.6%; Score 14; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
||
8 FH 9

RESULT 28

S65432
angiotensin I - horn fly (fragment)

C:Species: Haematobia irritans (horn fly)

C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65432
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elyin, C.; Kemp, D.; Willadsen, P.
Eur. J. Biochem. 237, 414-423, 1996
A:Title: Cloning and characterization of angiotensin-converting enzyme from the dipteran
A:Reference number: S65431; MUID:96215437; PMID:8647080
A:Accession: S65432
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-10 <MI>
A>Note: the source is designated as Haematobia irritans exigua

Query Match 28.6%; Score 14; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
||
8 FH 9

RESULT 29

B56899
serum heterodimer, 24k chain - sandbar shark (fragment)
C:Species: Carcharias plumbeus (sandbar shark)
C>Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 20-Jun-2000
C:Accession: B56899
R:Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
Comp. Biochem. Physiol. B 103, 563-568, 1992
A:Title: Purification of a novel heterodimer from shark (Carcharias plumbeus) serum by
A:Reference number: A56899; MUID:93092592; PMID:1458832
A:Accession: B56899
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <VAZ>
C:Keywords: glycoprotein; plasma

Query Match 28.6%; Score 14; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RVIKD 8
||
6 RVINE 10

RESULT 30

A90345
angiotensin precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
C:Accession: A90345; A01250
R:Elliot, D.F.; Peart, W.S.
Biochem. J. 65, 246-254, 1957
A:Title: The amino acid sequence in a hypertensin.
A:Reference number: A90345
A:Accession: A90345
A:Molecule type: protein
A:Residues: 1-10 <ELL>
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <AN1>
F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 28.6%; Score 14; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
||
8 FH 9

RESULT 31

S65387

cytochrome-c oxidase (EC 1.9.3.1) chain VII b, cardiac - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999

C/Accession: S65387, S65386

R/Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A/Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term

A/Reference number: S65372; MUID:95324529; PMID:7601105

A/Accession: S65387

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <SC>

A/Accession: S65386

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <SC2>

C/Keywords: cardiac muscle; heart; oxidoreductase

Query Match

Best Local Similarity 28.6%; Score 14; DB 2; Length 10;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3

DB 9 FH 10

RESULT 32

G42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003

C/Accession: G42762

R/Dick, L.R.; Moornaw, C.R.; Pramanik, B.C.; Demartino, G.N.; Slaughter, C.A.

Biochemistry 31, 7347-7355, 1992

A/Title: Identification and localization of a cysteine1 residue critical for the trypsin

A/Reference number: A42762; MUID:92378961; PMID:11510924

A/Accession: G42762

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-11 <DIC>

A/Note: sequence extracted from NCBI backbone (NCBIP:112176)

C/Superfamily: multicatalytic endopeptidase complex chain C9

C/Keywords: hydrolase

Query Match

Best Local Similarity 28.6%; Score 14; DB 2; Length 11;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 VIKDF 9

DB 2 VTDF 6

RESULT 33

PQ0733

unidentified 6.0/15K protein [imported] - rice (fragment)

C/Species: Oryza sativa (rice)

C/Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C/Accession: PQ0733

R/Komatsu, S.; Kajiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A/Title: A rice protein library; a data-file of rice proteins separated by two-dimension

A/Reference number: PQ0696

A/Accession: PQ0733

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-11 <KOM>

Query Match

Best Local Similarity 28.6%; Score 14; DB 2; Length 11;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVI 6

DB 1 HTII 4

RESULT 34

I54193

Rhesus blood group CcE protein - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000

C/Accession: I54193

R/Cherif-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Colin, Y.

Genomics 19, 68-74, 1994

A/Title: Organization of the gene (RHCE) encoding the human blood group RhCCE antigens

A/Reference number: I54193; MUID:94245182; PMID:8188244

A/Accession: I54193

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-11 <RES>

A/Cross-references: GB:S70456; NID:G546795; PIDN:AAD14061.1; PID:G4261761

C/Genetic:

A/Genes: GDB:RHCE

A/Cross-references: GDB:229957; OMIM:111700

A/Map position: 1p36.2-1p34

Query Match

Best Local Similarity 28.6%; Score 14; DB 2; Length 11;

Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KPRRVIX 7

DB 4 KYPRSVR 10

RESULT 35

PND042

stathmin - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998

C/Accession: PND042

R/Kato, H.

Kawasaki Igakkaishi 22, 245-259, 1996

A/Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro

A/Reference number: PND041

A/Accession: PND042

A/Molecule type: protein

A/Residues: 1-11 <KAT>

A/Experimental source: neuroblastoma cell

C/Comment: The molecular mass is 17,500 and the pI is 5.63. The amino-terminus is blocked

C/Keywords: brain

Query Match

Best Local Similarity 28.6%; Score 14; DB 2; Length 11;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 IKDF 9

DB 3 VPDF 6

RESULT 36

PH1376

T antigen variant K-3 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000

C/Accession: PH1376

R/Will, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.

J. Exp. Med. 176, 449-457, 1992

A/Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for the

A/Reference number: PH1373; MUID:92364547; PMID:1380062

A/Accession: PH1376

A:Status: preliminary
A:Molecule type: RNA
A:Residues: 1-11 <LIL>

Query Match 28.6%; Score 14; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 VIKDF 9
| | |
| | |
Db 4 VNKEF 8

RESULT 37
S09082

protease chain 1 - rat (fragment)
N:Alternate names: multicatalytic proteinase chain 1

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998

C:Accession: S09082
R:Lilley, K.S.; Davison, M.D.; Rivett, A.J.

FBMS Lett. 262, 327-329, 1990

A:Title: N-terminal sequence similarities between components of the multicatalytic protease

A:Reference number: S09082; MUID:90242957; PMID:2335214

A:Accession: S09082

A:Molecule type: Protein

A:Residues: 1-12 <LIL>
C:Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 28.6%; Score 14; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 VIKD 8
| | |
| | |
Db 7 VYKD 10

RESULT 38
G44644

neurotoxin-associated protein type B Rn+ 35K chain, band 3b - Clostridium botulinum (first

C:Species: Clostridium botulinum

C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C:Accession: G44644

R:Somers, E.; DasGupta, B.R.

J. Protein Chem. 10, 415-425, 1991

A:Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he

A:Reference number: A44644; MUID:92143938; PMID:1781887

A:Contents: type B

A:Accession: G44644

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <SOM>

A>Note: sequence extracted from NCBI backbone (NCBI:83785)

C:Keywords: hemagglutinin

Query Match 28.6%; Score 14; DB 2; Length 13;
Best Local Similarity 14.3%; Pred. No. 1.5e+04;
Matches 1; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FHRVIXD 8
| | |
| | |
Db 4 YONLMD 10

RESULT 39
S36887

ribosomal protein S14 - Mycobacterium bovis (fragments)

C:Species: Mycobacterium bovis

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

C:Accession: S36887

R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.

FBMS Lett. 331, 9-14, 1993

A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36887
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-23-12;13 <OHA>
C:Keywords: protein biosynthesis; ribosome

Query Match 28.6%; Score 14; DB 2; Length 13;
Best Local Similarity 20.0%; Pred. No. 1.5e+04;
Matches 1; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 4 RVIXD 8
| | |
| | |
Db 4 KIVKN 8

RESULT 40
PN0168

phosphopyruvate hydratase (EC 4.2.1.11) - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 11-Nov-1994

C:Accession: PN0168

R:Fukaya, N.; Chow, L.P.; Sugiyama, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.

submitted to JIPID, May 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi

A:Reference number: PN0160

A:Accession: PN0168

A:Molecule type: protein

A:Residues: 1-13 <FKX>
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 28.6%; Score 14; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 FHRVIXD 8
| | |
| | |
Db 6 FARVYD 12

RESULT 41
H85575

hypothetical protein 20899 [imported] - Escherichia coli (strain O157:H7, substrain EDL9;

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: H85575

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew

Hiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MUID:21074935; PMID:11206551

A:Accession: H85575

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <SNO>

A:Cross-references: GB:AB005174; NID:912513665; PTDN:ABG55068.1; GSPDB:GN00145; UWGP:Z08

A:Experimental source: strain O157:H7, substrain EDL933

C:Genetics:

A:Gene: Z0899

Query Match 28.6%; Score 14; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
| |
| |
Db 12 FH 13

RESULT 42
PQ0152

16S iron-sulfur protein - Chlamydomonas reinhardtii chloroplast (fragment)

N:Alternate names: frxB, hmoC10J
 C:Species: Chloroplast Chlamydomonas reinhardtii
 C:/Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-Sep-1993
 C:/Accession: P00152
 R:/Wu, M.; Nie, Z.Q.; Yang, J.
 Plant Cell 1, 551-557, 1989
 A:/Title: The 18-kD protein that binds to the chloroplast DNA replicative origin is an
 A:/Reference number: P00152; MUID:92404720; PMID:2562513
 A:/Accession: P00152
 A:/Molecule type: Protein
 A:/Residues: 1-14 <WUM>
 C:/Genetics:
 A:/Genome: chloroplast
 C:/Keywords: chloroplast

Query Match 28.6%; Score 14; DB 2; Length 14;
 Best Local Similarity 28.6%; Pred. No. 1.6e+04;
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 HRV1KDF 9
 | | | |
 Db 5 HTEFKNY 11

RESULT 43
 A61308 hemocyanin chain 2 - Sahara scorpion (fragment)
 C:/Species: Androctonus australis (Sahara scorpion)
 C:/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C:/Accession: A61308
 R:/Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
 FEBS Lett. 106, 289-291, 1979
 A:/Title: Structural characterization of seven different subunits in Androctonus australis
 A:/Reference number: A61308; MUID:80047238; PMID:499512
 A:/Accession: A61308
 A:/Status: Preliminary
 A:/Molecule type: Protein
 A:/Residues: 1-14 <JOL>

Query Match 28.6%; Score 14; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 1.6e+04;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KFRV1KDF 9
 | | | |
 Db 5 KODRIPLF 13

RESULT 44
 S29486 GTP-binding protein o-rab3 - electric ray (Discopyge ommata) (fragment)
 C:/Species: Discopyge ommata
 C:/Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C:/Accession: S29486
 R:/Volkhardt, W.; Pevsner, J.; Biferink, L.A.; Scheller, R.H.
 FEBS Lett. 317, 53-56, 1993
 A:/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicle
 A:/Reference number: S29485; MUID:93154521; PMID:8428634
 A:/Accession: S29486
 A:/Status: Preliminary
 A:/Molecule type: Protein
 A:/Residues: 1-14 <VOL>

Query Match 28.6%; Score 14; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 FHRV1 6
 | | | |
 Db 9 PNAVI 13

RESULT 45

G33160
 H+-transporting two-sector ATPase (EC 3.6.3.14) 9K chain - rat (fragment)
 C:/Species: Rattus norvegicus (Norway rat)
 C:/Date: 08-Mar-1991 #sequence_revision 08-Mar-1991 #text_change 03-Jun-2002
 C:/Accession: G33160
 R:/Godinot, C.
 submitted to the Protein Sequence Database, February 1991
 A:/Reference number: A33160
 A:/Accession: G33160
 A:/Status: preliminary
 A:/Molecule type: Protein
 A:/Residues: 1-14 <GOD>
 C:/Keywords: hydrolase

Query Match 28.6%; Score 14; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KFR 4
 | | | |
 Db 11 KFR 14

Search completed: August 30, 2004, 10:58:46
 Job time : 5.70608 secs

Thu Sep 2 07:41:29 2004

us-09-720-469a-1.aug30.rapb

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: August 30, 2004, 10:49:45 ; Search time 11.0668 Seconds

(without alignments)
257.253 Million cell updates/sec

Title: US-09-720-469A-1

Perfect score: 49

Sequence: 1 KFRHVIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1297172 seqs, 314612898 residues

Total number of hits satisfying chosen parameters: 149443

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	100.0	9	US-10-447-161-84	Sequence 84, Appl
2	49	100.0	9	US-10-788-016-1	Sequence 1, Appl
3	29	59.2	14	US-10-405-339-47	Sequence 47, Appl
4	28	57.1	12	US-10-601-953-76	Sequence 76, Appl
5	28	57.1	14	US-10-601-953-77	Sequence 77, Appl
6	27	55.1	10	US-09-851-138-204	Sequence 204, Appl
7	26	53.1	9	US-09-984-056-61	Sequence 61, Appl
8	26	53.1	9	US-09-984-056-62	Sequence 62, Appl
9	26	53.1	9	US-09-984-057-61	Sequence 61, Appl
10	26	53.1	9	US-09-984-057-62	Sequence 62, Appl
11	26	53.1	9	US-10-105-232-61	Sequence 61, Appl
12	26	53.1	9	US-10-105-232-62	Sequence 62, Appl
13	26	53.1	9	US-10-189-437-61	Sequence 61, Appl
14	26	53.1	9	US-10-189-437-62	Sequence 62, Appl
15	25	51.0	11	US-10-293-822-14	Sequence 14, Appl

16	25	51.0	11	US-10-293-822-22	Sequence 22, Appl
17	25	51.0	12	US-10-601-953-64	Sequence 64, Appl
18	25	51.0	14	US-10-601-953-65	Sequence 65, Appl
19	24	49.0	9	US-10-211-207-23	Sequence 23, Appl
20	24	49.0	9	US-10-211-207-24	Sequence 24, Appl
21	24	49.0	9	US-10-077-106-23	Sequence 23, Appl
22	24	49.0	9	US-10-077-106-24	Sequence 24, Appl
23	24	49.0	14	US-10-105-232-270	Sequence 270, Appl
24	24	49.0	14	US-10-189-437-257	Sequence 257, Appl
25	23	46.9	9	US-09-834-765-139	Sequence 139, Appl
26	23	46.9	9	US-09-834-765-419	Sequence 419, Appl
27	23	46.9	10	US-09-834-765-477	Sequence 477, Appl
28	23	46.9	10	US-09-834-765-666	Sequence 666, Appl
29	23	46.9	11	US-09-984-056-72	Sequence 72, Appl
30	23	46.9	11	US-09-984-057-72	Sequence 72, Appl
31	23	46.9	11	US-10-105-232-72	Sequence 266, Appl
32	23	46.9	11	US-10-105-232-266	Sequence 266, Appl
33	23	46.9	11	US-10-189-437-72	Sequence 253, Appl
34	23	46.9	11	US-10-189-437-253	Sequence 874, Appl
35	23	46.9	13	US-10-253-286-874	Sequence 85, Appl
36	23	46.9	13	US-10-325-810-85	Sequence 85, Appl
37	23	46.9	13	US-10-044-639-85	Sequence 85, Appl
38	23	46.9	13	US-10-044-639-85	Sequence 85, Appl
39	23	46.9	13	US-10-245-871-874	Sequence 28, Appl
40	23	46.9	14	US-10-014-340-28	Sequence 2, Appl
41	23	46.9	14	US-10-190-264-2	Sequence 135, Appl
42	22	44.9	9	US-09-820-053A-135	Sequence 135, Appl
43	22	44.9	9	US-10-109-171-135	Sequence 500, Appl
44	22	44.9	10	US-09-876-904A-500	Sequence 114, Appl
45	22	44.9	10	US-09-833-039-114	

ALIGNMENTS

RESULT 1
US-10-447-161-84
; Sequence 84, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-84

Query Match 100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 KFRHVIKDF 9
|||||

RESULT 2
US-10-788-016-1
; Sequence 1, Application US/10788016
; Publication No. US20040141992A1
; GENERAL INFORMATION:
; APPLICANT: ITOH, Kyogo
; TITLE OF INVENTION: Desensitizers

FILE REFERENCE: 3190-049
CURRENT APPLICATION NUMBER: US/10/788,016
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: PCT/JP02/08641
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: JP P2001-260046
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 84th residue
OTHER INFORMATION: to the 92nd residue of cyclophilin B
US-10-788-016-1

Query Match 100.0%; Score 49; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KFHVIKDF 9
DB 1 KFHVIKDF 9

RESULT 3
US-10-405-339-47
Sequence 47, Application US/10405339
Publication No. US20030190364A1
GENERAL INFORMATION:
APPLICANT: Panitch, Alyssa
TITLE OF INVENTION: Biological Affinity Based Delivery Systems
FILE REFERENCE: 9138-007905
CURRENT APPLICATION NUMBER: US/10/405,339
CURRENT FILING DATE: 2003-04-01
PRIOR APPLICATION NUMBER: US 60/369,568
PRIOR FILING DATE: 2002-04-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-10-405-339-47

Query Match 59.2%; Score 29; DB 14; Length 14;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 FHRVVKDF 9
DB 1 FHRVVKDF 8

RESULT 4
US-10-601-953-76
Sequence 76, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Therapeutic Compounds
FILE REFERENCE: 02-0305
CURRENT APPLICATION NUMBER: US/10/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28

NUMBER OF SEQ ID NOS: 900
SOFTWARE: PatentIn version 3.2
SEQ ID NO 76
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-601-953-76

Query Match 57.1%; Score 28; DB 16; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRIKDF 9
DB 1 HRIKDF 7

RESULT 5
US-10-601-953-77
Sequence 77, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
APPLICANT: Quay, Steven C.
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
FILE REFERENCE: 02-0305
CURRENT APPLICATION NUMBER: US/10/601,953
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOFTWARE: PatentIn version 3.2
SEQ ID NO 77
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-601-953-77

Query Match 57.1%; Score 28; DB 16; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRIKDF 9
DB 2 HRIKDF 8

RESULT 6
US-09-851-118-204
Sequence 204, Application US/09851138
Publication No. US20020183508A1
GENERAL INFORMATION:
APPLICANT: MAERTENS, GEERT
STUYVER, LIEVEN
TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
AGENTS
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSER: ARNOLD, WHITE & DURKEE
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

Thu Sep 2 07:41:29 2004

us-09-720-469a-1.aug30.rapb

Page 3

```
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 6.0 / ASCII text output
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/851.138
FILING DATE: 09-May-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/836.075
FILING DATE: <Unknown>
APPLICATION NUMBER: EP 94870166.9
FILING DATE: 21 Oct 1994
APPLICATION NUMBER: EP 95870076.7
FILING DATE: 28 Jun 1995
ATTORNEY/AGENT INFORMATION:
NAME: KAMMERER, PATRICIA A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: INNS:004
INFORMATION FOR SEQ ID NO: 204:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 204:
US-09-851-138-204
```

```
Query Match
Best Local Similarity 55.1%; Score 27; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 7
US-09-984-056-61
Sequence 61, Application US/09984056
Patent No. US20020120106A1
GENERAL INFORMATION:
APPLICANT: BOGOCCH, ELENORE S.
TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
FILE REFERENCE: 09425-46903
CURRENT APPLICATION NUMBER: US/09/984,056
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentln 2.1
SEQ ID NO 61
LENGTH: 9
TYPE: PRT
ORGANISM: Polyoma virus
US-09-984-056-61
```

```
Query Match
Best Local Similarity 53.1%; Score 26; DB 9; Length 9;
Best Local Similarity 52.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 8

```
US-09-984-056-62
Sequence 62, Application US/09984056
Patent No. US20020120106A1
GENERAL INFORMATION:
APPLICANT: BOGOCCH, ELENORE S.
TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
FILE REFERENCE: 09425-46903
CURRENT APPLICATION NUMBER: US/09/984,056
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 103
SOFTWARE: Patentln 2.1
SEQ ID NO 62
LENGTH: 9
TYPE: PRT
ORGANISM: Polyoma virus
US-09-984-056-62
```

```
Query Match
Best Local Similarity 53.1%; Score 26; DB 9; Length 9;
Best Local Similarity 52.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
RESULT 9
US-09-984-057-61
Sequence 61, Application US/09984057
Patent No. US20020151677A1
GENERAL INFORMATION:
APPLICANT: BOGOCCH, ELENORE S.
TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
FILE REFERENCE: 09425-46902
CURRENT APPLICATION NUMBER: US/09/984,057
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: Patentln 2.1
SEQ ID NO 61
LENGTH: 9
TYPE: PRT
ORGANISM: Polyoma virus
US-09-984-057-61
```

```
Query Match
Best Local Similarity 53.1%; Score 26; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 8

Db 1 KQHRLEKD 8

RESULT 10

US-09-984-057-62

; Sequence 62, Application US/09984057

; Patent No. US20030151677A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLICIN AND METHODS OF IDENTIFYING

; TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES

; FILE REFERENCE: 09425-46902

; CURRENT APPLICATION NUMBER: US/09/984,057

; CURRENT FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: 60/303,396

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 09/146,755

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: 09/817,144

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 08/198,139

; PRIOR FILING DATE: 1994-02-17

; NUMBER OF SEQ ID NOS: 90

; SOFTWARE: PatentIn 2.1

; SEQ ID NO: 62

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Polyoma virus

US-09-984-057-62

Query Match 53.1%; Score 26; DB 9; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.2e+06; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2;

Qy 1 KHRVYKD 8

Db 1 KQHRLEKD 8

RESULT 11

US-10-105-232-61

; Sequence 61, Application US/10105232

; Publication No. US20030180328A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS

; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS

; FILE REFERENCE: 09425-46904

; CURRENT APPLICATION NUMBER: US/10/105,232

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/303,396

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 09/146,755

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: 09/817,144

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 08/198,139

; PRIOR FILING DATE: 1994-02-17

; NUMBER OF SEQ ID NOS: 535

; SOFTWARE: PatentIn 2.1

; SEQ ID NO: 61

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Polyoma virus

US-10-105-232-61

Query Match 53.1%; Score 26; DB 14; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.2e+06; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2;

Qy 1 KHRVYKD 8

Db 1 KQHRLEKD 8

RESULT 12

US-10-105-232-62

; Sequence 62, Application US/10105232

; Publication No. US20030180328A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS

; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS

; FILE REFERENCE: 09425-46904

; CURRENT APPLICATION NUMBER: US/10/105,232

; CURRENT FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 60/303,396

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 09/146,755

; PRIOR FILING DATE: 1998-09-04

; PRIOR APPLICATION NUMBER: 09/817,144

; PRIOR FILING DATE: 2001-03-27

; PRIOR APPLICATION NUMBER: 08/198,139

; PRIOR FILING DATE: 1994-02-17

; NUMBER OF SEQ ID NOS: 535

; SOFTWARE: PatentIn 2.1

; SEQ ID NO: 62

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Polyoma virus

US-10-105-232-62

Query Match 53.1%; Score 26; DB 14; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.2e+06; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2;

Qy 1 KHRVYKD 8

Db 1 KQHRLEKD 8

RESULT 13

US-10-189-437-61

; Sequence 61, Application US/10189437

; Publication No. US2003019441A1

; GENERAL INFORMATION:

; APPLICANT: BOGOCH, SAMUEL

; APPLICANT: BOGOCH, ELENORE S.

; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE

; TITLE OF INVENTION: AND IN INFLUENZA EPIDEMICS

; FILE REFERENCE: 09425/46905

; CURRENT APPLICATION NUMBER: US/10/189,437

; CURRENT FILING DATE: 2002-07-08

; PRIOR APPLICATION NUMBER: 10/105,232

; PRIOR FILING DATE: 2002-03-26

; PRIOR APPLICATION NUMBER: 09/984,057

; PRIOR FILING DATE: 2001-10-26

; PRIOR APPLICATION NUMBER: 60/303,396

; PRIOR FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: 60/278,761

; PRIOR FILING DATE: 2001-03-27

; NUMBER OF SEQ ID NOS: 729

; SOFTWARE: PatentIn 2.1

; SEQ ID NO: 61

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Polyoma virus

US-10-189-437-61

```
Query Match 53.1%; Score 25; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KHRVIXD 8
| | | |
| | | |
Db 1 KHRVIXD 8

RESULT 14
US-10-189-437-62
; Sequence 62, Application US/10189437
; Publication No. US20030194414A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCCH, SAMUEL
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFOR
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; PRIOR FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Polyoma virus
US-10-189-437-62

Query Match 53.1%; Score 26; DB 14; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KHRVIXD 8
| | | |
| | | |
Db 1 KHRVIXD 8

RESULT 15
US-10-293-822-14
; Sequence 14, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/10/293,822
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/418,780
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-822-14

Query Match 51.0%; Score 25; DB 14; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 2 FHRVIX 7
| | | |
| | | |
Db 1 YKRIK 6

RESULT 16
US-10-293-822-22
; Sequence 22, Application US/10293822
; Publication No. US20030083470A1
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-043001
; CURRENT APPLICATION NUMBER: US/10/293,822
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/418,780
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01782
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JAPAN 9/116402
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-293-822-22

Query Match 51.0%; Score 25; DB 14; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FHRVIX 7
| | | |
| | | |
Db 1 YKRIK 6

RESULT 17
US-10-601-953-64
; Sequence 64, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; PRIOR FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-64

Query Match 51.0%; Score 25; DB 16; Length 12;
Best Local Similarity 42.9%; Pred. No. 4.3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HRVIXDF 9
| | | |
| | | |
Db 1 HGIRDF 7

RESULT 18
```

US-10-601-953-65
 ; Sequence 65, Application US/10601953
 ; Publication No. US2004007540A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Quay, Steven C.
 ; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
 ; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
 ; TITLE OF INVENTION: Therapeutic Compounds
 ; FILE REFERENCE: 02-0305
 ; CURRENT APPLICATION NUMBER: US/10/601,953
 ; CURRENT FILING DATE: 2003-06-24
 ; PRIOR APPLICATION NUMBER: 60/392,512
 ; PRIOR FILING DATE: 2002-06-28
 ; NUMBER OF SEQ ID NOS: 900
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 65
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic construct
 US-10-601-953-65

Query Match 51.0%; Score 25; DB 16; Length 14;
 Best Local Similarity 42.9%; Pred. No. 5e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 9
 ||:||||
 DB 2 HGLRDF 8

RESULT 19
 US-10-211-207-23
 ; Sequence 23, Application US/10211207
 ; Publication No. US20030004113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Collins, Mary
 ; APPLICANT: Madrenas, Joaquin
 ; APPLICANT: Carrero, Beatriz
 ; APPLICANT: Kuchroo, Vijay
 ; TITLE OF INVENTION: METHODS FOR MODULATING THE INTERACTION BETWEEN CTLA4 AND
 ; TITLE OF INVENTION: RESPONSES BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
 ; TITLE OF INVENTION: PP2A
 ; FILE REFERENCE: GNN-027
 ; CURRENT APPLICATION NUMBER: US/10/211,207
 ; CURRENT FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: US/10/077,106
 ; PRIOR FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 23
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Polyomavirus small
 US-10-211-207-23

Query Match 49.0%; Score 24; DB 14; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 8
 ||:||||
 DB 1 HRELKD 6

RESULT 20
 US-10-211-207-24
 ; Sequence 24, Application US/10211207
 ; Publication No. US20030004113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Collins, Mary
 ; APPLICANT: Madrenas, Joaquin

; APPLICANT: Carrero, Beatriz
 ; APPLICANT: Kuchroo, Vijay
 ; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
 ; TITLE OF INVENTION: RESPONSES BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
 ; TITLE OF INVENTION: PP2A
 ; FILE REFERENCE: GNN-027
 ; CURRENT APPLICATION NUMBER: US/10/211,207
 ; CURRENT FILING DATE: 2002-08-02
 ; PRIOR APPLICATION NUMBER: US/10/077,106
 ; PRIOR FILING DATE: 2002-02-15
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 24
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Polyomavirus medium
 US-10-211-207-24

Query Match 49.0%; Score 24; DB 14; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 8
 ||:||||
 DB 1 HRELKD 6

RESULT 21
 US-10-077-106-23
 ; Sequence 23, Application US/10077106
 ; Publication No. US20030166531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Collins, Mary
 ; APPLICANT: Madrenas, Joaquin
 ; APPLICANT: Carrero, Beatriz
 ; APPLICANT: Kuchroo, Vijay
 ; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
 ; TITLE OF INVENTION: RESPONSES BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
 ; TITLE OF INVENTION: PP2A
 ; FILE REFERENCE: GNN-027
 ; CURRENT APPLICATION NUMBER: US/10/077,106
 ; CURRENT FILING DATE: 2002-02-15
 ; PRIOR APPLICATION NUMBER: 60/269,757
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO: 23
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Polyomavirus small
 US-10-077-106-23

Query Match 49.0%; Score 24; DB 14; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.2e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRV1KD 8
 ||:||||
 DB 1 HRELKD 6

RESULT 22
 US-10-077-106-24
 ; Sequence 24, Application US/10077106
 ; Publication No. US20030166531A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Collins, Mary
 ; APPLICANT: Madrenas, Joaquin
 ; APPLICANT: Carrero, Beatriz
 ; APPLICANT: Kuchroo, Vijay
 ; TITLE OF INVENTION: METHODS FOR MODULATING AN IMMUNE
 ; TITLE OF INVENTION: RESPONSES BY MODULATING THE INTERACTION BETWEEN CTLA4 AND
 ; TITLE OF INVENTION: PP2A

FILE REFERENCE: GNN-027
CURRENT APPLICATION NUMBER: US/10/077,106
CURRENT FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: 60/269,757
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 9
TYPE: PRT
ORGANISM: Polyomavirus medium
US-10-077-106-24

Query Match 49.0%; Score 24; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIR 8
| : |||
Db 1 HREIKD 6

RESULT 23

US-10-105-232-270
Sequence 270, Application US/10105232
Publication No. US20030180326A1
GENERAL INFORMATION:
APPLICANT: BOGOCCH, SAMUEL
APPLICANT: BOGOCCH, ELEONORE S.
TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
FILE REFERENCE: 09425-46904
CURRENT APPLICATION NUMBER: US/10/105,232
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 535
SOFTWARE: PatentIn 2.1
SEQ ID NO 270
LENGTH: 14
TYPE: PRT
ORGANISM: Influenza virus
US-10-105-232-270

Query Match 49.0%; Score 24; DB 14; Length 14;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KHRVIR 7
| : |||
Db 1 KLRVIR 7

RESULT 24
US-10-189-437-257
Sequence 257, Application US/10189437
Publication No. US2003019441A1
GENERAL INFORMATION:
APPLICANT: BOGOCCH, SAMUEL
APPLICANT: BOGOCCH, ELEONORE S.
TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
FILE REFERENCE: 09425/46905
CURRENT APPLICATION NUMBER: US/10/189,437
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 10/105,232

PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: 09/984,057
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 729
SOFTWARE: PatentIn 2.1
SEQ ID NO 257
LENGTH: 14
TYPE: PRT
ORGANISM: Influenza virus
US-10-189-437-257

Query Match 49.0%; Score 24; DB 14; Length 14;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KHRVIR 7
| : |||
Db 1 KLRVIR 7

RESULT 25
US-09-834-765-139
Sequence 139, Application US/09834765
Patent No. US20020055478A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Pia M. Challita-Bid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE OF INVENTION: AND DETECTION OF CANCER
FILE REFERENCE: 129.6USU1
CURRENT APPLICATION NUMBER: US/09/834,765
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 139
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-765-139

Query Match 46.9%; Score 23; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FHRVIR 9
| : |||
Db 1 YHRVIR 8

RESULT 26
US-09-834-765-419
Sequence 419, Application US/09834765
Patent No. US20020055478A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Pia M. Challita-Bid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
TITLE OF INVENTION: AND DETECTION OF CANCER
FILE REFERENCE: 129.6USU1

```

; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 419
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-419
```

```

Query Match          46.9%; Score 23; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FHRVYKDF 9
       : |||:|
Db      2 YEHVYKNF 9
```

```

RESULT 27
US-09-834-765-477
; Sequence 477, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Chalilta-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 477
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-477
```

```

Query Match          46.9%; Score 23; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FHRVYKDF 9
       : |||:|
Db      2 YEHVYKNF 9
```

```

RESULT 28
US-09-834-765-666
; Sequence 666, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Chalilta-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Ava Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129.6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
```

```

; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO: 666
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-666
```

```

Query Match          46.9%; Score 23; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 FHRVYKDF 9
       : |||:|
Db      3 YEHVYKNF 10
```

```

RESULT 29
US-09-984-056-72
; Sequence 72, Application US/09984056
; Patent No. US20020120106A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICONS AND METHODS OF USE
; FILE REFERENCE: 09425-46903
; CURRENT APPLICATION NUMBER: US/09/984,056
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
; PRIOR FILING DATE: 1998-09-04
; PRIOR FILING DATE: 1994-02-17
; PRIOR APPLICATION NUMBER: 09/817,144
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 08/198,139
; PRIOR FILING DATE: 1994-02-17
; NUMBER OF SEQ ID NOS: 103
; SOFTWARE: PatentIn 2.1
; SEQ ID NO: 72
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-984-056-72
```

```

Query Match          46.9%; Score 23; DB 9; Length 11;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 HREVIK 7
       : |||:|
Db      7 HRLIK 11
```

```

RESULT 30
US-09-984-057-72
; Sequence 72, Application US/09984057
; Patent No. US20020151677A1
; GENERAL INFORMATION:
; APPLICANT: BOGOCH, SAMUEL
; APPLICANT: BOGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICONS AND METHODS OF IDENTIFYING
; TITLE OF INVENTION: REPLICIN-CONTAINING SEQUENCES
; FILE REFERENCE: 09425-46902
; CURRENT APPLICATION NUMBER: US/09/984,057
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/146,755
```

;; PRIOR FILING DATE: 1998-09-04
;; PRIOR APPLICATION NUMBER: 09/817,144
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: 08/198,139
;; PRIOR FILING DATE: 1994-02-17
;; NUMBER OF SEQ ID NOS: 90
;; SOFTWARE: PatentIn 2.1
;; SEQ ID NO 72
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-984-057-72

Query Match 46.9%; Score 23; DB 9; Length 11;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
||:|
Db 7 HRLIK 11

RESULT 31

US-10-105-232-72
;; Sequence 72, Application US/10105232
;; Publication No. US20030180328A1
;; GENERAL INFORMATION:
;; APPLICANT: BOGOCH, SAMUEL
;; APPLICANT: BOGOCH, ELENORE S.
;; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
;; FILE REFERENCE: 09425-46904
;; CURRENT APPLICATION NUMBER: US/10/105,232
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: 60/303,396
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: 60/278,761
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: 09/146,755
;; PRIOR FILING DATE: 1998-09-04
;; PRIOR APPLICATION NUMBER: 09/817,144
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: 08/198,139
;; PRIOR FILING DATE: 1994-02-17
;; NUMBER OF SEQ ID NOS: 535
;; SOFTWARE: PatentIn 2.1
;; SEQ ID NO 72
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-105-232-72

Query Match 46.9%; Score 23; DB 14; Length 11;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
||:|
Db 7 HRLIK 11

RESULT 32

US-10-105-232-266
;; Sequence 266, Application US/10105232
;; Publication No. US20030180328A1
;; GENERAL INFORMATION:
;; APPLICANT: BOGOCH, SAMUEL
;; APPLICANT: BOGOCH, ELENORE S.
;; TITLE OF INVENTION: REPLICIN PEPTIDES IN RAPID REPLICATION OF GLIOMA CELLS
;; FILE REFERENCE: 09425-46904
;; CURRENT APPLICATION NUMBER: US/10/105,232
;; CURRENT FILING DATE: 2002-03-26

;; PRIOR APPLICATION NUMBER: 60/303,396
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: 60/278,761
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: 09/146,755
;; PRIOR FILING DATE: 1998-09-04
;; PRIOR APPLICATION NUMBER: 09/817,144
;; PRIOR FILING DATE: 2001-03-27
;; PRIOR APPLICATION NUMBER: 08/198,139
;; PRIOR FILING DATE: 1994-02-17
;; NUMBER OF SEQ ID NOS: 535
;; SOFTWARE: PatentIn 2.1
;; SEQ ID NO 266
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Influenza virus
;; FEATURE:
;; NAME/KEY: MOD_RES
;; LOCATION: (8)
;; OTHER INFORMATION: gly or gln
US-10-105-232-266

Query Match 46.9%; Score 23; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KFRVIR 7
||:|
Db 5 KFXIEX 11

RESULT 33

US-10-189-437-72
;; Sequence 72, Application US/10189437
;; Publication No. US2003019441A1
;; GENERAL INFORMATION:
;; APPLICANT: BOGOCH, SAMUEL
;; APPLICANT: BOGOCH, ELENORE S.
;; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
;; FILE REFERENCE: 09425/46905
;; CURRENT APPLICATION NUMBER: US/10/189,437
;; PRIOR FILING DATE: 2002-07-08
;; PRIOR APPLICATION NUMBER: 10/105,232
;; PRIOR FILING DATE: 2002-03-26
;; PRIOR APPLICATION NUMBER: 09/984,057
;; PRIOR FILING DATE: 2001-10-26
;; PRIOR APPLICATION NUMBER: 60/303,396
;; PRIOR FILING DATE: 2001-07-09
;; PRIOR APPLICATION NUMBER: 60/278,761
;; PRIOR FILING DATE: 2001-03-27
;; NUMBER OF SEQ ID NOS: 729
;; SOFTWARE: PatentIn 2.1
;; SEQ ID NO 72
;; LENGTH: 11
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-189-437-72

Query Match 46.9%; Score 23; DB 14; Length 11;
Best Local Similarity 80.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIR 7
||:|
Db 7 HRLIK 11

RESULT 34

US-10-189-437-253
;; Sequence 253, Application US/10189437
;; Publication No. US2003019441A1
;; GENERAL INFORMATION:
;; APPLICANT: BOGOCH, SAMUEL

APPLICANT: BOGUCH, ELENORE S.
TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFOR
FILE REFERENCE: 09425/46905
CURRENT APPLICATION NUMBER: US/10/189,437
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: 10/105,232
PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: 09/984,057
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 729
SOFTWARE: PatentIn 2.1
SEQ ID NO: 253
LENGTH: 11
TYPE: PRT
ORGANISM: Influenza virus
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (8)
OTHER INFORMATION: gly or gln
US-10-189-437-253

Query Match 46.9%; Score 23; DB 14; Length 11;
Best Local Similarity 57.1%; Pred. No. 9.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KHRVIX 7
||| : |
DB 5 KRMXIK 11

RESULT 35
US-10-253-286-874
Sequence 874, Application US/10253286
Publication No. US20040058881a1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: IL-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2015
CURRENT APPLICATION NUMBER: US/10/253,286
CURRENT FILING DATE: 2003-01-13
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 905
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 874
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: IL-key/PLP epitope hybrid peptide
FEATURE:
OTHER INFORMATION: C-term amidated
US-10-253-286-874

Query Match 46.9%; Score 23; DB 12; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 KHRVIX 9
||| : |
DB 4 KRLPIAIF 12

RESULT 36
US-10-325-810-85

Sequence 85, Application US/10325810
Publication No. US20030204069A1
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Langner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/325,810
FILING DATE: 20-Dec-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181
FILING DATE: 29-Sep-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Auehhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Peptide
LOCATION: 1..13
OTHER INFORMATION: /note="telomerase RT palm, primer grip
motif C peptide from Schistosomacnaryces
pombe trf"
SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-10-325-810-85

Query Match 46.9%; Score 23; DB 12; Length 13;

Thu Sep 2 07:41:29 2004

us-09-720-469a-1.aug30.rapb

Page 11

Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 RVKDF 9
||: ||
Db 4 RVVDF 9

RESULT 37

US-10-044-692-85
; Sequence 85, Application US/10044692
; Publication No. US20030096344A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,692

FILING DATE: 11-Jan-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..13

OTHER INFORMATION: /note= "telomerase RT palm, primer grip motif C peptide from Schizosaccharomyces pombe RT"

SEQUENCE DESCRIPTION: SEQ ID NO: 85:

US-10-044-692-85

Query Match 46.9%; Score 23; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 RVKDF 9
||: ||
Db 4 RVVDF 9

RESULT 38
US-10-044-539-85
; Sequence 85, Application US/10044539
; Publication No. US2003010093A1
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin

Andrews, William H.

TITLE OF INVENTION: HUMAN TELOMERASE CATALYTIC SUBUNIT: DIAGNOSTIC AND THERAPEUTIC METHODS

NUMBER OF SEQUENCES: 335

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/044,539

FILING DATE: 11-Jan-2002

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/912,951

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 015389-002600US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Peptide

LOCATION: 1..13

OTHER INFORMATION: /note= "telomerase RT palm, primer grip"

motif C peptide from Schizosaccharomyces
pombe RTT"
SEQUENCE DESCRIPTION: SEQ ID NO: 85;
US-10-044-539-85

Query Match 46.9%; Score 23; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RVKDF 9
||:|:
Db 4 RVDVDF 9

RESULT 39
US-10-245-871-874
; Sequence 874, Application US/10245871
; Publication No. US20030235594A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: 11-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2013
; CURRENT APPLICATION NUMBER: US/10/245,871
; PRIOR FILING DATE: 2003-01-09
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 874
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; OTHER INFORMATION: 11-key/PLP epitope hybrid peptide
; OTHER INFORMATION: C-term amidated
US-10-245-871-874

Query Match 46.9%; Score 23; DB 15; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 KFHRIKDF 9
||:|:
Db 4 KFHRIKDF 12

RESULT 40
US-10-014-340-28
; Sequence 28, Application US/10014340
; Publication No. US2003006411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 28
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-28

Query Match 46.9%; Score 23; DB 12; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIND 8
||:|:
Db 2 HQVED 7

RESULT 41
US-10-190-264-2
; Sequence 2, Application US/10190264
; Publication No. US20030082631A1
; GENERAL INFORMATION:
; APPLICANT: Gustavsson, Anna-Lena
; APPLICANT: Svensson, Stefan
; APPLICANT: Uppenberg, Jonas
; TITLE OF INVENTION: COMPOUNDS MODULATING PPAR-GAMMA
; FILE REFERENCE: 13425-118001
; CURRENT APPLICATION NUMBER: US/10/190,264
; CURRENT FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/304,706
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: SE 0102384-5
; PRIOR FILING DATE: 2001-07-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-264-2

Query Match 46.9%; Score 23; DB 14; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRVIND 8
||:|:
Db 8 HRVIND 13

RESULT 42
US-09-820-053A-135
; Sequence 135, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-135

Query Match 44.9%; Score 22; DB 10; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KFHRIKDF 9
||:|:
Db 1 KFHRIKDF 9

RESULT 43
US-10-109-171-135

Thu Sep 2 07:41:29 2004

us-09-720-469a-1.aug30.rapb

Page 13

```
; Sequence 135, Application US/10109171
; Publication No. US20030109452a1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 135
; LENGTH: 9
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: AMIDATION
US-10-109-171-135

Query Match
Best Local Similarity 44.9%; Score 22; DB 14; Length 9;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KFHRYIKP 9
Db 1 KFKLAKKF 9

RESULT 44
US-09-876-904A-500
; Sequence 500, Application US/09876904A
; Publication No. US20030072794a1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONTIGUATES INTO TARGETED LIPOsome COMPLEXES
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Yeast SNF2, a transcriptional regulator of many
; OTHER INFORMATION: genes.
US-09-876-904A-500

Query Match
Best Local Similarity 44.9%; Score 22; DB 10; Length 10;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFHRYIK 7
Db 3 RIHKVIR 9

RESULT 45
US-09-833-039-114
; Sequence 114, Application US/09833039
; Publication No. US20030175960A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
```

```
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 114
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-114

Query Match
Best Local Similarity 44.9%; Score 22; DB 10; Length 10;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KFHRYI 6
Db 5 RIHKVIR 10
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Search completed: August 30, 2004, 11:04:51
Job time : 12.0068 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 8.66554 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-1

Perfect score: 49

Sequence: 1 KFHRIKDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP archaea:*
- 2: SP bacteria:*
- 3: SP fungi:*
- 4: SP human:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_mhc:*
- 8: SP_organelle:*
- 9: SP_phase:*
- 10: SP_plant:*
- 11: SP_proteus:*
- 12: SP_virus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*
- 15: SP_virus:*
- 16: SP_bacteriopl:*
- 17: SP_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	51.0	14	Q9UNM9	Q9UNM9 homo sapien
2	23	46.9	10	Q9TQV4	Q9TQV4 equus caball
3	22	44.9	13	P87031	P87031 saccharomyc
4	21	42.9	8	Q8AWW0	Q8AWW0 coscoroba c
5	21	42.9	8	Q8AWV9	Q8AWV9 anser caeru
6	21	42.9	8	Q8AWV8	Q8AWV8 cygnus colu
7	21	42.9	8	Q8AWV7	Q8AWV7 anas platyr
8	20	40.8	8	Q05403	Q05403 saccharomyc
9	19	38.8	10	Q8N6B1	Q8N6B1 homo sapien
10	19	38.8	11	Q9XSP7	Q9XSP7 pygathrix n
11	19	38.8	11	Q9XSP2	Q9XSP2 hylobates s
12	19	38.8	11	Q9XSP5	Q9XSP5 pan troglod
13	19	38.8	11	Q9XSP8	Q9XSP8 presbytis j
14	19	38.8	11	Q9XSP6	Q9XSP6 pongo pygma
15	19	38.8	11	Q9XSQ4	Q9XSQ4 gorilla gor
16	19	38.8	13	Q80XX0	Q80XX0 cricetus

Result 1	ID	Q9UNM9	PRELIMINARY;	PRT;	14 AA.	Q5379 rhodobacter
AC	Q9UNM9	01-MAY-2000 (TReMBLrel. 13, Created)				Q9LW7 manduca sex
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)					Q8171 pseudomonas
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)					Q91X4 vibrio chol
DE	RING3 protein (Fragment).					Q9UP7 homo sapien
GN	RING3.					Q95179 homo sapien
OS	Homo sapiens (Human).					Q35792 saccharomyc
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					Q80191 newcasle d
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					Q9131 callitrix
OX	NCBI_TaxID=9606;					Q9129 saginus oe
RN	[1]					Q91Y5 mus musculu
RP	SEQUENCE FROM N.A.					Q47693 escherichia
RA	Kedache M, Zhang F, Greenberg D.A.;					Q91CS1 bacillus su
RT	"A Dinucleotide Repeat Between Exons 2 and 3 of the Human RING3 Gene."					Q81Y9 chroococcid
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.					Q82W9 yerisla pe
DR	EMBL; AF107699; AAd2463.1; -					Q91E8 toxoplasma
DR	InterPro; IPR001487; Bromodomain.					Q91E8 sclerocium
FT	NON_TER	1				Q91E8 pichia anqu
FT	NON_TER	14				Q91E8 homo sapien
FT	SEQUENCE	14 AA; 1677 MW; 5CDP03680AE22D3 CRC64;				Q16234 homo sapien

Query Match 51.0%; Score 25; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

Q9TQV4	Q9TQV4	PRELIMINARY;	PRT;	10 AA.
AC	Q9TQV4			
DT	01-MAY-2000 (TReMBLrel. 13, Created)			

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE POP-variant * transferrin gene, EXON 17 and partial CDS (Fragment).
 OS Equus caballus (Horse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Giffard J.M., Brandon R.B., Bell T.K.;
 RT "Further identification of single nucleotide polymorphisms in the
 RT equine transferrin gene."
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF185778; AAF05491.1; -
 DR EMBL; AF185770; AAF05483.1; -
 DR EMBL; AF185771; AAF05484.1; -
 DR EMBL; AF185772; AAF05485.1; -
 DR EMBL; AF185773; AAF05486.1; -
 DR EMBL; AF185774; AAF05487.1; -
 DR EMBL; AF185775; AAF05488.1; -
 DR EMBL; AF185776; AAF05489.1; -
 DR EMBL; AF185777; AAF05490.1; -
 FT NON_TER
 SQ SEQUENCE 10 AA; 1188 MW; 6DF67DE9D1AE8DD CRC64;

Query Match 46.9%; Score 23; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 FHRV 5
 DB 7 FHRV 10

RESULT 3
 ID P87031 PRELIMINARY; PRT; 13 AA.
 AC P87031;

DT 01-JUN-1997 (TREMBLrel. 04, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE ORF YGR126W (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Van Dyck L., Skala J., de Wergifosse P., Purnelle B., Talia E.,
 RA Nawrocki A., Del Bino S., Goffeau A.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 FT NON_TER
 SQ SEQUENCE 13 AA; 1594 MW; 2954BA87F3F8C9C8 CRC64;

Query Match 44.9%; Score 22; DB 3; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

CY 2 FHRV 5
 DB 8 FHRV 11

RESULT 4
 ID Q8AWMO PRELIMINARY; PRT; 8 AA.
 AC Q8AWMO;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE LDH-B (Fragment).
 OS Coscoroba coscoroba (Coscoroba swan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Coscoroba.
 OX NCBI_TaxID=8863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., Stojan J., Quinn T.W.;
 RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
 RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba
 RT coscoroba.".
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY123324; AAM96898.1; -
 FT NON_TER
 SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 42.9%; Score 21; DB 13; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 3 HRVND 8
 DB 2 HRVND 7

RESULT 5
 ID Q8AWV9 PRELIMINARY; PRT; 8 AA.
 AC Q8AWV9;

DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE LDH-B (Fragment).
 OS Anser caerulescens caerulescens (snow goose).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anser.
 OX NCBI_TaxID=70340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., Stojan J., Quinn T.W.;
 RT "Isolation of a Precisely Delineated, Recently Transposed Chicken
 RT Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba
 RT coscoroba.".
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY123325; AAM96899.1; -
 FT NON_TER
 SQ SEQUENCE 8 AA; 911 MW; D73AADC2C05331F1 CRC64;

Query Match 42.9%; Score 21; DB 13; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

CY 3 HRVND 8
 DB 2 HRVND 7

RESULT 6
 ID Q8AWV8 PRELIMINARY; PRT; 8 AA.
 AC Q8AWV8;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE LDH-B (Fragment).
 GN LDH-B.
 OS Cygnus columbianus (tundra swan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromia; Aves; Neognathae; Anseriformes; Anatidae; Cynus.
 OX NCBI_TaxID=110926;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., Stron J., Quinn T.W.;
 RT "Isolation of a precisely delineated, Recently Transposed Chicken
 Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba
 coscoroba.";
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY123326; AAM96900.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 911 MW; D73AAC2C05331F1 CRC64;

Query Match 42.9%; Score 21; DB 13; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRVTD 8
 DB 2 HKIVAD 7

RESULT 7

ID O8AW7 PRELIMINARY; PRT; 8 AA.
 AC O8AW7;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE LDH-B (Fragment).
 GN LDH-B.
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauromia; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cotter J.-P., Stron J., Quinn T.W.;
 RT "Isolation of a precisely delineated, Recently Transposed Chicken
 Repeat 1 (CRI) Retrotransposon Within an Intron of the Coscoroba
 coscoroba.";
 RL Submitted (JUN-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY123327; AAM96901.1; -.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 911 MW; D73AAC2C05331F1 CRC64;

Query Match 42.9%; Score 21; DB 13; Length 8;
 Best Local Similarity 33.3%; Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRVTD 8
 DB 2 HKIVAD 7

RESULT 8

ID O05403 PRELIMINARY; PRT; 8 AA.
 AC O05403;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE DNA for ORF's from chromosome XV (Fragment).
 OS Saccharomyces cerevisiae (Baker's Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;

RX MEDLINE=96021609; PubMed=8533473;
 RA Zumbstein E., Pearson B.M., Kallgeropoulos A., Schweizer M.;
 RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains
 RT more than twice as many unknown as known open reading frames.";
 RL Yeast 11:975-986(1995).
 DR EMBL; X63121; CAA58183.1; -.
 FT NON_TER 8
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C441E058 CRC64;

Query Match 40.8%; Score 20; DB 3; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRVTD 7
 DB 3 HNVVK 7

RESULT 9

ID O8N6B1 PRELIMINARY; PRT; 10 AA.
 AC O8N6B1;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Capacitative calcium channel protein Trp1 (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Late pregnancy myometrium;
 RX MEDLINE=22181008; PubMed=12193412;
 RA Yang M., Gupta A., Shlykov S.G., Corrigan B., Tsujimoto S.,
 RA Sanborn B.M.;
 RT "Multiple Trp isoforms implicated in capacitative calcium entry are
 RT expressed in human pregnant myometrium and myometrial cells.";
 RL Biol. Reprod. 67:988-994(2002).
 DR EMBL; AF483546; AAM97861.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1336 MW; 0DD0C0B401F40724 CRC64;

Query Match 38.8%; Score 19; DB 4; Length 10;
 Best Local Similarity 80.0%; Pred. No. 4.4e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRVTD 7
 DB 6 HRDIX 10

RESULT 10

ID O9XSP7 PRELIMINARY; PRT; 11 AA.
 AC O9XSP7;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Pygathrix nemaeus (Dove langur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Pygathrix.
 OX NCBI_TaxID=54133;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598912;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AF243282; CAB45924.1; -.

FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 38.8%; Score 19; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIR 7
 DB 7 HRSVK 11

RESULT 11

ID Q9XSP2 PRELIMINARY; PRT; 11 AA.
 AC Q9XSP2;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Hylobates syndactylus (Siayang) (Symphalangus syndactylus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylodactylidae; Hylodactylidae;
 OC NCBI_TaxID=9590;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243280; CAB45927.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 38.8%; Score 19; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIR 7
 DB 7 HRSVK 11

RESULT 12

ID Q9XSP5 PRELIMINARY; PRT; 11 AA.
 AC Q9XSP5;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
 OC NCBI_TaxID=9598;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243277; CAB45926.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101E1E044 CRC64;

Query Match 38.8%; Score 19; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIR 7
 DB 7 HRSVK 11

RESULT 13

ID Q9XSP8 PRELIMINARY; PRT; 11 AA.
 AC Q9XSP8;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Presbytis johni.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Colobinae;
 OC Presbytis.
 OC NCBI_TaxID=98375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243281; CAB46013.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 38.8%; Score 19; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIR 7
 DB 7 HRSVK 11

RESULT 14

ID Q9XSP6 PRELIMINARY; PRT; 11 AA.
 AC Q9XSP6;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain (Fragment).
 GN PDGFA.
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pongo.
 OC NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20065871; PubMed=10598812;
 RA Bonthron D.T., Smith S.L., Campbell R.;
 RT "Complex patterns of intragenic polymorphism at the PDGFA locus."
 RL Hum. Genet. 105:452-459(1999).
 DR EMBL; AJ243279; CAB45925.1; -.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1345 MW; 7FB881F101E1E044 CRC64;

Query Match 38.8%; Score 19; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIR 7
 DB 7 HRSVK 11


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RESULT 15
Q9XSQ4 ID Q9XSQ4 PRELIMINARY; PRT; 11 AA.
AC Q9XSQ4;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DE Platelet-derived growth factor A chain (Fragment).
GN PDGFA.
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Gorilla.
OX NCBI_Taxid=9593;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20065871; PubMed=10598812;
RA Bonthron D.T., Smith S.L., Campbell R.;
RT "Complex patterns of intragenic polymorphism at the PDGFA locus.";
RL Hum. Genet. 105:452-459(1989).
DR EMBL, AJ243278; CAB45916.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1331 MW; 7FB881F101B1F2D4 CRC64;

Query Match
Best Local Similarity 38.8%; Score 19; DB 6; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRVIR 7
DB 7 HRSVK 11

RESULT 16
Q80XX0 ID Q80XX0 PRELIMINARY; PRT; 13 AA.
AC Q80XX0;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DE Hypoxanthine phosphoribosyl transferase (Fragment).
GN Hprt.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.
OX NCBI_Taxid=10029;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93024555; PubMed=1383700;
RA Fuscoe J.C., Zimmerman L.J., Fekete A., Setzer R.W., Rossiter B.J.;
RT "Analysis of X-ray-induced Hprt mutations in CHO cells: insertion and
RT deletions.";
RL Molec. Res. 269:171-183(1992).
DR EMBL, S46270; AAP1884.1; -.
KW GO; GO:0016740; F:transferase activity; IEA.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1516 MW; 113A46B0848F760 CRC64;

Query Match
Best Local Similarity 38.8%; Score 19; DB 11; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HRVIR 8
DB 8 HGVIMD 13

RESULT 17
Q53579 ID Q53579 PRELIMINARY; PRT; 12 AA.
AC Q53579;

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DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PufA.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_Taxid=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHI- and LHI+ Rhodospirillum rubrum pufA
RT mutants.";
RL J. Bacteriol. 174:3030-3041(1992).
DR EMBL, S97551; AAC60405.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1627 MW; 0F92F6E8A70532B CRC64;

Query Match
Best Local Similarity 36.7%; Score 18; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 8.4e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFERV 5
DB 3 KFYKI 7

RESULT 18
Q9TXX7 ID Q9TXX7 PRELIMINARY; PRT; 9 AA.
AC Q9TXX7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Juvenile hormone binding protein, JHBP=4.9 kDa GIU-C peptide
DE (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Spingioidea;
OC Spingidae; Spinginae; Manduca.
OX NCBI_Taxid=7130;
RN [1]
RP SEQUENCE.
RX MEDLINE=92134256; PubMed=1734862;
RA Tschura K., Prestwich G.D.;
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
RT binding protein.";
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 9 AA; 1023 MW; E063C40045A2D401 CRC64;

Query Match
Best Local Similarity 34.7%; Score 17; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRV 5
DB 2 HRV 4

RESULT 19
Q8RUF1 ID Q8RUF1 PRELIMINARY; PRT; 10 AA.
AC Q8RUF1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Porin-like protein (Fragment).
DE Pseudomonas fluorescens.
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

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OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC16-2, TCC29-5, and TC97;
RC TRANSPOSOME=TM5041A1, TM5041B, and TM5041D1;
RA Kholodil G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
RT "Distribution of distinct microvariants of TM5041 in environmental
  bacteria."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ422128; CAD19527.1; -
DR EMBL; AJ422130; CAD19529.1; -
FT NON_TER 10
SQ SEQUENCE 10 AA; 1206 MW; 23C47E7401F5A417 CRC64;

Query Match 34.7%; Score 17; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 HRVIR 7
DB 6 HRPFR 10

RESULT 20
OY 0931X4 PRELIMINARY; PRT; 10 AA.
AC 0931X4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE MiOC (Moic) (Fragment).
GN MiOC.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=O395;
RA Saha A., Hazalalka S., Bhadra R.K.;
RT "Cloning and characterization of the origin of replication of
  chromosome 1 of Vibrio cholerae."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SG24;
RA Saha A., Hazalalka S., Bhadra R.K.;
RT "Characterization of the oric region of Vibrio cholerae chromosome
  1."
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY034431; AK61370.1; -
DR EMBL; AY211526; AA053341.1; -
FT NON_TER 1
SQ SEQUENCE 10 AA; 1303 MW; 464F014042D40337 CRC64;

Query Match 34.7%; Score 17; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 RVIKDF 9
DB 5 RVINRF 10

RESULT 21
OY 09UBP7 PRELIMINARY; PRT; 13 AA.
AC 09UBP7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

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DE Inosine monophosphatase 2 (Fragment).
GN IMPA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Detera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP19p, maps to a
  susceptibility region for bipolar disorder."
RL Mol. Psychiatry 2:393-397 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigan M., Karkera J.D., Sharma M., Berruttini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
  2."
RL Mol. Psychiatry 5:165-171 (2000).
DR EMBL; AF025882; AAD22136.1; -
DR EMBL; AF025881; AAD22136.1; JOINED.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;

Query Match 34.7%; Score 17; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 HRVIR 8
DB 6 HRPFR 11

RESULT 22
OY 095179 PRELIMINARY; PRT; 14 AA.
AC 095179;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Glucose-6-phosphatase hydrolytic subunit (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156747; PubMed=10024523;
RA Schmol D., Waser C., Hinde C.J., Allan B.B., Walther R.,
RA Burchell A.;
RT "Identification of a cAMP response element within the glucose-6-
  phosphate hydrolytic subunit gene promoter which is involved in the
  transcriptional regulation by cAMP and glucocorticoids in H4IIE
  hepatoma cells."
RL Biochem. J. 338:457-463 (1999).
DR EMBL; AF051355; AAD11621.1; -
FT NON_TER 14
SQ SEQUENCE 14 AA; 1666 MW; A6B78EF997FFD46 CRC64;

Query Match 34.7%; Score 17; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 VIKDF 9
DB 9 VIKDF 13

RESULT 23

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Q35792
ID Q35792 PRELIMINARY; PRT; 8 AA.
AC Q35792;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Inside intron 3 (Fragment)
OS Saccharomyces cerevisiae (Baker's yeast).
OC Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=273-10B; PubMed=6254986;
RX MEDLINE=81069885;
RA Bonitz S.G.; Coruzzi G.; Thalenfeld B.; Tzagoloff A.; Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
RT nucleotide sequence of the gene coding for subunit 1 of yeast
RT cytochrome oxidase."
RL J Biol Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24063.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 8
FT NON_TER 8 1
SQ SEQUENCE 8 AA; 1025 MW; 084693345B5A337 CRC64;

Query Match 32.7%; Score 16; DB 8; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKDF 9
DB 1 LKDY 4

RESULT 24
Q35792 PRELIMINARY; PRT; 8 AA.
ID Q35792;
AC Q35792;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE HN/HNO (Fragment).
GN HN/HNO.
OS Newcastle disease virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Rubulavirus.
OX NCBI_TaxID=11176;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94175786; PubMed=8129624;
RA Collins M.S.; Strong I.; Alexander D.J.;
RT "Evaluation of the molecular basis of pathogenicity of the variant
RT Newcastle disease viruses termed 'pigeon PMV-1 viruses'."
RL Arch. Virol. 134:403-411(1994).
DR EMBL; S69419; AAI9628.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 929 MW; 33D4087AA337205B CRC64;

Query Match 32.7%; Score 16; DB 12; Length 8;
Best Local Similarity 50.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKID 8
DB 2 ILKD 5

RESULT 25
Q9TT31 PRELIMINARY; PRT; 12 AA.
ID Q9TT31

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AC Q9TT31;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Beta-globin (Fragment).
OS Callithrix jacchus (Common marmoset).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20188801; PubMed=10723742;
RA Francino M.P.; Ochman H.;
RT "Strand Symmetry around the beta-globin Origin of Replication in
RT Primates."
RL Mol. Biol. Evol. 17:416-422(2000).
DR EMBL; AF205413; AAF23764.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1251 MW; 07BC8AFAB8D72DD4 CRC64;

Query Match 32.7%; Score 16; DB 6; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFH 3
DB 10 KYH 12

RESULT 26
Q9TT29 PRELIMINARY; PRT; 12 AA.
ID Q9TT29;
AC Q9TT29;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Beta-globin (Fragment).
OS Saguinus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
OX NCBI_TaxID=490;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=20188801; PubMed=10723742;
RA Francino M.P.; Ochman H.;
RT "Strand Symmetry around the beta-globin Origin of Replication in
RT Primates."
RL Mol. Biol. Evol. 17:416-422(2000).
DR EMBL; AF205415; AAF23766.1; -.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1251 MW; 07BC8AFAB8D72DD4 CRC64;

Query Match 32.7%; Score 16; DB 6; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFH 3
DB 10 KYH 12

RESULT 27
Q91YF5 PRELIMINARY; PRT; 12 AA.
ID Q91YF5;
AC Q91YF5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GMS synthase protein (Fragment).
GN GMS SYNTHASE.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RA Shuichi T.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18020; CAC79652.1; -.

FT NON TER 12
 SQ SEQUENCE 12 AA; 1445 MW; 84E7876609572735 CRC64;

Query Match
 Best Local Similarity 32.7%; Score 16; DB 11; Length 12;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 VKXD 8
 Db 7 LIKD 10

RESULT 28

ID Q47693 PRELIMINARY; PRT; 13 AA.

AC Q47693;

DT 01-NOV-1996 (TRENBLREL. 01, Created)

DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)

DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)

DE Elongation factor TU (EF-TU) (Fragment).

GN TUFB.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RP SEQUENCE FROM N.A.

RX MEDLINE=82080657; PubMed=7312036;

RA Hudson L., Rossi J., Landy A.;

RL "Dual function transcripts specifying tRNA and mRNA.";

DR EMBL; X04181; CAA27777.1; -.

DR GO; GO:0003746; P:translation elongation factor activity; IEA.

KM Elongation factor; Protein biosynthesis.

FT NON TER 13
 SQ SEQUENCE 13 AA; 1617 MW; C433B82A18DB19 CRC64;

Query Match
 Best Local Similarity 32.7%; Score 16; DB 2; Length 13;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KFER 4
 Db 5 KFER 8

RESULT 29

ID Q91CS1 PRELIMINARY; PRT; 14 AA.

AC Q91CS1;

DT 01-OCT-2000 (TRENBLREL. 15, Created)

DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)

DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)

DE Levan sucrase (Fragment).

GN SABC.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1423;

RP SEQUENCE FROM N.A.
 RA Maldonado R., Casadesus J.;

RT "Identification of IS210 in *Acetobacter vinelandii*: a novel.

RT functional insertion element member of the IS5 family.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ249381; CAB76429.1; -.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.

KM Plasmid.

FT NON TER 14

FT NON TER 14

SQ SEQUENCE 14 AA; 1623 MW; 8DC9108BA1B18745 CRC64;

Query Match
 Best Local Similarity 32.7%; Score 16; DB 2; Length 14;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 VKXD 8
 Db 8 LIKD 11

RESULT 30

ID Q8LIY9 PRELIMINARY; PRT; 14 AA.

AC Q8LIY9;

DT 01-OCT-2002 (TRENBLREL. 22, Created)

DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)

DT 01-OCT-2002 (TRENBLREL. 22, Last annotation update)

DE Proteolysis-inducing tag (Fragment).

OS Chroococcidiopsis sp. PCC 6712.

OC Bacteria; Cyanobacteria; Pleurocapsales; Chroococcidiopsis.

OX NCBI_TaxID=118675;

RP SEQUENCE FROM N.A.

RX MEDLINE=21970088; PubMed=11972342;

RA Williams K.P.;

RL "Descent of a split RNA.";

DR EMBL; AY082650; AAM03309.1; -.

FT NON TER 1

SQ SEQUENCE 14 AA; 1607 MW; DB3C06BC6C20E19 CRC64;

Query Match
 Best Local Similarity 32.7%; Score 16; DB 2; Length 14;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KFER 4
 Db 6 KFER 9

RESULT 31

ID Q8ZDW9 PRELIMINARY; PRT; 14 AA.

AC Q8ZDW9;

DT 01-MAR-2002 (TRENBLREL. 20, Created)

DT 01-MAR-2002 (TRENBLREL. 20, Last sequence update)

DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)

DE Phenylalanyl-tRNA synthetase operon leader peptide (phenylalanyl-tRNA synthetase (pheS) operon leader peptide).

GN PHEM OR YPO2429A OR Y1906.

OS Yersinia pestis.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Yersinia.

OX NCBI_TaxID=632;

RP SEQUENCE FROM N.A.

RX MEDLINE=21470413; PubMed=11586360;

RA Parkhill U., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Felwell T., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 Staley S.C., McDonough K.A., Nilles M.L., Mason J.S., Blattner F.R.,
 Perry R.D.;
 RT "Genome sequence of Yersinia pestis KIM."
 RL J. Bacteriol. 184:4601-4611(2002).
 DR EMBL; AJ414152; CAC91234.1; -;
 DR EMBL; AE013793; AAM85473.1; -;
 DR PIR; AF0296; AF0296.
 DR GO; GO:0004812; F:RNA ligase activity; IEA.
 KW Aminoacyl-tRNA synthetase; Complete proteome.
 SQ SEQUENCE 14 AA; 1813 MW; 6141D61506FFFD4 CRC64;

Query Match 32.7%; Score 16; DB 16; Length 14;
 Best Local Similarity 57.1%; Pred. No. 2.4e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 HRVTKDF 9
 DB 2 HTVIRF 8

RESULT 32
 O9N6M5 PRELIMINARY; PRT; 8 AA.
 ID O9N6M5
 AC O9N6M5
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE Dihydrofolate reductase thymidylate synthase (Fragment).
 GN F01.
 OS Toxoplasma gondii.
 OC Buxariota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
 OC Toxoplasma.
 OX NCBI_TaxID=5811;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RH, CONGAR TC751G34, SEA OTTER TC0826G1, and BEVERLEY;
 RA Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;
 RT "Strain typing of Toxoplasma gondii: Comparison of Antigen-Coding and
 RT Housekeeping Genes."
 RL J. Parasitol. 0:0-0(2000).
 DR EMBL; AF249695; AAF79153.1; -;
 DR EMBL; AF249692; AAF79150.1; -;
 DR EMBL; AF249693; AAF79151.1; -;
 DR EMBL; AF249694; AAF79152.1; -;
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 8 AA; 1035 MW; 33C9AAA05B133044 CRC64;
 Query Match 30.6%; Score 15; DB 5; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 IKDF 9
 DB 5 IDDF 8

RESULT 33
 O9UR18 PRELIMINARY; PRT; 9 AA.
 ID O9UR18
 AC O9UR18
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Translation elongation factor 1-alpha (Fragment).
 GN EFL-ALPHA.
 OS Sclerotium cepivorum.
 OC Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Sclerotium.
 OX NCBI_TaxID=38492;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DE-2, and DE-1;
 RA Couch B.C., Kohn L.M.;
 RT "Clonal spread of Sclerotium cepivorum in onion production with
 RT evidence of past recombination events."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBD databases.
 DR EMBL; AF163671; AAD46912.1; -;
 DR EMBL; AF163670; AAD46911.1; -;
 DR GO; GO:0003746; F:translation elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1178 MW; 619C19C3B1041B4 CRC64;

Query Match 30.6%; Score 15; DB 3; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 RVTKDF 9
 DB 2 RTTEKF 7

RESULT 34
 O47569 PRELIMINARY; PRT; 11 AA.
 ID O47569
 AC O47569
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=X-12;
 RX MEDLINE=94162733; PubMed=7764507;
 RA Yamada M., Yanai S., Talkuder A.;
 RT "Analysis of products of the Escherichia coli genomic genes and
 RT regulation of their expressions: an applicable procedure for genomic
 RT analysis of other microorganisms."
 RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
 DR EMBL; D21156; BAA04692.1; -;
 KW Hypothetical protein.
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1332 MW; C0B8E40E37672732 CRC64;
 Query Match 30.6%; Score 15; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 3e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 HRVY 6
 DB 2 HOVL 5

RESULT 35
 O9UR95 PRELIMINARY; PRT; 11 AA.
 ID O9UR95
 AC O9UR95
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
 DE Heat shock protein 60 homolog (Fragment).

OS *Pichia angusta* (Yeast) (*Hansenula polymorpha*).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; *Pichia*.
 CX NCBI_TaxID=4905;
 RN [1]

RP MEDLINE=9522840; PubMed=8096822;
 RA Evers M.E., Huhse B., Titorenko V.I., Kunau W.H., Hartl F.U.,
 RA Harder W., Veenhuis M.,
 RT "Affinity purification of molecular chaperones of the yeast *Hansenula*
 RT *polymorpha* using immobilized denatured alcohol oxidase.";
 RL FEBS Lett. 321:32-36(1993).
 SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C372B CRC64;

Query Match 30.6%; Score 15; DB 3; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3e+04;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

CY 3 HRVIR 7
 DB 2 HKELK 6

RESULT 36

ID Q9UNL8 PRELIMINARY; PRT; 11 AA.
 AC Q9UNL8;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
 DE APC2 protein (Fragment).
 GN APC2
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Carr I.M., Markham A.F., Colleta P.L., Wai L., Ashman J., Morrison E.,
 RA Meredith D.M.,
 RT "APC2 partial gene sequence."
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF110338; AAD29275.1; -.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1326 MW; 75881D7BB441EAB4 CRC64;

Query Match 30.6%; Score 15; DB 4; Length 11;
 Best Local Similarity 40.0%; Pred. No. 3e+04;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

CY 4 RVIR 8
 DB 1 QVLRD 5

RESULT 37

ID Q16234 PRELIMINARY; PRT; 11 AA.
 AC Q16234;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Hud protein (Fragment).
 GN HUD.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94349312; PubMed=8069866;
 RA Sekido Y., Bader S.A., Carbone D.P., Johnson B.E., Minna J.D.;

RT "Molecular analysis of the Hud gene encoding a paraneoplastic
 RT encephalomyelitis antigen in human lung cancer cell lines."
 RL Cancer Res. 54:4988-4992(1994).
 DR EMBL; S73887; AAD14142.1; -.
 DR PIR; I52708; I52708.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1289 MW; 2EDCF20E204415N7 CRC64;

Query Match 30.6%; Score 15; DB 4; Length 11;
 Best Local Similarity 50.0%; Pred. No. 3e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

CY 4 RVIR 7
 DB 6 RILK 9

RESULT 38

ID Q8WEL7 PRELIMINARY; PRT; 11 AA.
 AC Q8WEL7;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Sida hookeriana.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Malvales; Malvaceae; Malvoideae; Sida.
 CX NCBI_TaxID=108446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.,
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384624; AAM50396.1; -.
 DR GO; GO:0009507; Chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 KFRH 4
 DB 7 KOHR 10

RESULT 39

ID Q8WEM2 PRELIMINARY; PRT; 11 AA.
 AC Q8WEM2;
 DT 01-OCT-2002 (TRENBLREL. 22, Created)
 DT 01-OCT-2002 (TRENBLREL. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Lagunaria patersonia.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Malvales; Malvaceae; Malvoideae; Lagunaria.
 CX NCBI_TaxID=183274;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.,
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using

RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384616; AAM50388.1; -
 GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFR 4
 |||
 Db 7 KOHR 10

RESULT 40

Q8MES5 PRELIMINARY; PRT; 11 AA.
 ID Q8MES5;
 AC Q8MES5;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 GN Rpl16.
 OS Abelsonchus manihot.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvaceae; Abelsonchus.
 OC NCBI_TaxID=183220;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384561; AAM50399.1; -
 GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFR 4
 |||
 Db 7 KOHR 10

RESULT 41

Q8MEP0 PRELIMINARY; PRT; 11 AA.
 ID Q8MEP0;
 AC Q8MEP0;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 GN Rpl16.
 OS Hibiscus perrubus.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvaceae; Hibiscus.
 OC NCBI_TaxID=183256;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384598; AAM50370.1; -
 GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384598; AAM50370.1; -
 GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1470 MW; 7227C351D32409D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFR 4
 |||
 Db 7 KOHR 10

RESULT 42

Q8MER8 PRELIMINARY; PRT; 11 AA.
 ID Q8MER8;
 AC Q8MER8;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 GN Rpl16.
 OS Dombeya tiliaacea.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Dombeyoideae; Dombeya.
 OC NCBI_TaxID=121875;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384569; AAM50407.1; -
 GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1424 MW; 7227C351D32A9D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFR 4
 |||
 Db 7 KOHR 10

RESULT 43

Q8MES1 PRELIMINARY; PRT; 11 AA.
 ID Q8MES1;
 AC Q8MES1;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DE 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 GN Rpl16.
 OS Alyogyne pinoniana.
 OC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids II; Malvales; Malvaceae; Malvaceae; Alyogyne.
 OC NCBI_TaxID=183226;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 RT chloroplast DNA sequences of ndhF and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384569; AAM50407.1; -
 GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1424 MW; 7227C351D32A9D4 CRC64;

RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhf and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384566; AAM50404.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MM; 7227C351D32409D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFH 4
 DB 7 KQHR 10

RESULT 44

Q8MEP3 PRELIMINARY; PRT; 11 AA.
 AC Q8MEP3; 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus normanii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhf and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384595; AAM50367.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MM; 7227C351D32409D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFH 4
 DB 7 KQHR 10

RESULT 45

Q8MEQ7 PRELIMINARY; PRT; 11 AA.
 AC Q8MEQ7; 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Ribosomal protein 16 (Fragment).
 GN RPL16.
 OS Hibiscus drummondii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Hibiscus.
 OX NCBI_TaxID=183239;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
 RT "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
 chloroplast DNA sequences of ndhf and the rpl16 intron."
 RL Syst. Bot. 27:333-350(2002).
 DR EMBL; AF384581; AAM50353.1; -
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1470 MM; 7227C351D32409D4 CRC64;

Query Match 30.6%; Score 15; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KFH 4
 DB 7 KQHR 10

Search completed: August 30, 2004, 10:55:09
 Job time : 12.665 secs

OX NCB1_TaxID=37700;

RP SEQUENCE FROM N.A. PubMed=9071198;

RA MEDLINE=94350802; Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.,

RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for

RL their classification.";

CC J. Bacteriol. 176:5244-5254 (1994).

CC -1- FUNCTION: Protein S19 forms a complex with S13 that binds strongly

CC to the 16S ribosomal RNA (By similarity) of ribosomal proteins.

CC -1- SIMILARITY: Belongs to the S19 family of ribosomal proteins.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC EMBL: L27036; AAA3946.1; -

CC HAMAP: MF_00531; -; 1.

CC InterPro: IPR002222; Ribosomal S19, PARTIAL.

CC PROSITE: PS00323; RIBOSOMAL S19, PARTIAL.

CC RIBOSOMAL PROTEIN; RNA-binding.

CC NON_TER 1

CC SEQUENCE 14 AA; 1668 MW; 8FD46FB830DFBBA CRC64;

Query Match 38.8%; Score 19; DB 1; Length 14;

Best Local Similarity 57.1%; Pred. No. 8.6e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FHRVTKD 8

DB 1 FHRVTKD 7

RESULT 3

TXL4_LOCMT STANDARD; PRT; 10 AA.

AC P30250;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Locustatachyrxinin IV (TK-IV).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;

OC Acridoidea; Acrididae; Cerdipodinae; Locusta.

OX NCB1_TaxID=7004;

RP SEQUENCE.

RP TISSUE=Brain;

RC MEDLINE=91219696; PubMed=2132575;

RA Schoofs L., Holman G.M., Hayes T.K., Kochansky J.P., Nachman R.J.,

RA de Loof A.;

RT "Locustatachyrxinin III and IV: two additional insect neuropeptides

RT with homology to peptides of the vertebrate tachykinin family.";

RL Regul. Pept. 31:199-212 (1990).

CC -1- FUNCTION: Myoactive peptide. Stimulates the contraction of the

CC oviduct and foregut.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC PIR: B60073; ECLQ4M.

DR Tachyrxinin; Neuropeptide; Amidation.

KW MOD_RES 10 AA; 1040 MW; 9E52CD71E9C87735 CRC64;

SEQUENCE 10 AA; 1040 MW; 9E52CD71E9C87735 CRC64;

Query Match 32.7%; Score 16; DB 1; Length 10;

Best Local Similarity 75.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRV 5

DB 6 FHRV 9

RESULT 4

ANGT_HORSE STANDARD; PRT; 14 AA.

AC P01016;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Angiotensinogen [contains: Angiotensin I (Ang I); Angiotensin II (Ang

DE II); Angiotensin III (Ang III) (Des-asp[1]-angiotensin II)]

DE (Fragment).

CC AGT OR SERPINA8.

CC Equus caballus (Horse).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

CC NCB1_TaxID=9796;

CC SEQUENCE.

CC Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;

CC "The preparation, purification, and amino acid sequence of a

CC polypeptide renin substrate.";

CC J. Exp. Med. 106:439-453 (1957).

CC -1- FUNCTION: In response to lowered blood pressure, the enzyme renin

CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin

CC converting enzyme) then removes a dipeptide to yield the

CC physiologically active peptide angiotensin II, the most potent

CC pressor substance known, which helps regulate volume and mineral

CC balance of body fluids.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

CC -1- SIMILARITY: Belongs to the serpin family.

CC PIR: A92775; A01250.

CC PDB: 1ER8; 15-OCT-91.

CC InterPro: IPR000215; Serpin.

CC PROSITE: PS00284; SERPIN, PARTIAL.

CC KM Vasocostrictor; Plasma; Serpin; 3D-structure.

CC PEPTIDE 1 10

CC PEPTIDE 1 8

CC PEPTIDE 2 8

CC NON_TER 14 14

CC SEQUENCE 14 AA; 1759 MW; 2E921F8E8FBD7 CRC64;

Query Match 32.7%; Score 16; DB 1; Length 14;

Best Local Similarity 40.0%; Pred. No. 3.3e+03;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRV 6

DB 8 FHLV 12

RESULT 5

GER1_HORVU STANDARD; PRT; 13 AA.

AC P28525;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Germin GSI (Fragment).

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

CC NCB1_TaxID=4513;

CC SEQUENCE.

CC STRAIN=CV. CM 72; TISSUE=Root;

RA Harkman W.J., Tao H.P., Tanaka C.K.;

RT "Germin-like polypeptides increase in barley roots during salt

stress.";

RL Plant Physiol. 97:366-374(1991).
 CC -1- FUNCTION: May play a role in altering the properties of cell
 CC walls during germinative growth.
 CC -1- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.
 CC -1- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in
 CC the mature region, but not in the tip. Not detected in leaves.
 CC -1- INDUCTION: Increased by salt stress in roots and decreased by salt
 CC stress in coleoptile.
 CC -1- PTM: Glycosylated.
 CC -1- SIMILARITY: Belongs to the germin family.
 DR InterPro: IPR001929; Germin.
 DR PROSITE: PS00725; GERMIN; PARTIAL.
 KW Apolact; Cell wall; Glycoprotein; Multigene family.
 FT UNSTR 10 10
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1470 MW; 43FB58AA3B7B6D7 CRC64;
 Query Match 30.6%; Score 15; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKDF 9
 Db 6 LQDF 9

RESULT 6
 ID GER2_HORVU STANDARD; PRT; 13 AA.
 AC P28526;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Germin GS2 (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. CM 72; TISSUE=Root;
 RA Huxman W.J., Tao H.P., Tanaka C.K.;
 RT "Germin-like polypeptides increase in barley roots during salt
 stress.";
 RL Plant Physiol. 97:366-374(1991).
 CC -1- FUNCTION: May play a role in altering the properties of cell walls
 CC during germinative growth.
 CC -1- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.
 CC -1- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the
 CC mature region, but not in the tip. Not detected in leaves.
 CC -1- INDUCTION: Increased by salt stress in roots and decreased by salt
 CC stress in coleoptile.
 CC -1- PTM: Glycosylated.
 CC -1- SIMILARITY: Belongs to the germin family.
 DR InterPro: IPR001929; Germin.
 DR PROSITE: PS00725; GERMIN; PARTIAL.
 KW Apolact; Cell wall; Glycoprotein; Multigene family.
 FT UNSTR 10 10
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1484 MW; 43FB5A1A3B7B6D7 CRC64;
 Query Match 30.6%; Score 15; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.8e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKDF 9
 Db 6 LQDF 9

RESULT 7
 ID LCK6_LEUMA STANDARD; PRT; 8 AA.
 AC P21143;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin IV (L-IV).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT "Primary structure and synthesis of two additional neuropeptides
 RT from Leucophaea maderae: members of a new family of
 RT cephalomyotropins.";
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -1- FUNCTION: This cephalomyotrophic peptide stimulates contractile
 CC activity of cockroach prothorax (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 KW Neuropeptide; Amidation.
 FT MOD RES 8
 FT MOD RPS 8
 SQ SEQUENCE 8 AA; 906 MW; DC6365B1E9D5BD8A CRC64;
 Query Match 28.6%; Score 14; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
 Db 4 FH 5

RESULT 8
 ID LCK6_LEUMA STANDARD; PRT; 8 AA.
 AC P19986;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin VI (L-VI).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;
 OC Blaberidae; Leucophaea.
 OX NCBI_TaxID=6988;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Head;
 RA MEDLINE=87052651; PubMed=2877794;
 RX Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure, and synthesis of leucokinin V and VI:
 RT myotrophic peptides of Leucophaea maderae.";
 RL Comp. Biochem. Physiol. 88C:27-30(1987).
 CC -1- FUNCTION: This cephalomyotrophic peptide stimulates contractile
 CC activity of cockroach prothorax (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- PTM: Glycosylated.
 DR PIR: JS0316; JS0316.
 KW Neuropeptide; Amidation; Pyroglutamate carboxylic acid.
 FT MOD RES 1 1
 FT MOD RPS 8
 FT MOD RPS 8
 SQ SEQUENCE 8 AA; 935 MW; 9D6365B1E9D5A5A6 CRC64;
 Query Match 28.6%; Score 14; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
CC 4 FH 5
DB 4 FH 5

RESULT 9
PAPA CALVO STANDARD; PRT; 9 AA.
AC P41865; (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 10.
RT CalliFMRamide 10.
OS CalliFMRamide 10.
CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
CC Calliphoridae; Calliphora.
NCBI_TaxID=27454;
RN 11
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
RA Renfeld U.F., Thorpe A.,
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the PARP (FMRamide related peptide)
CC family.
DR PIR; A44787; A44787.
KM Neuropeptide; Amidation.
FT MOD RES 9 AMIDATION.
FT UNSTRE 1 OR S OR A.
SQ SEQUENCE 9 AA; 1183 MW; 29D00699CAB40457 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDF 9
CC 4 RDF 6
DB 4 RDF 6

RESULT 10
FIBB PAPA STANDARD; PRT; 9 AA.
AC P19343;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen beta chain [contains: fibrinopeptide B] (Fragment).
GN FGB.
OS Papio hamadryas (Hamadryas baboon).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Buthera; Primates; Catarrhini; Cercopitheidae;
CC Cercopitheidae; Papio.
NCBI_TaxID=9557;
RN 11
RP SEQUENCE.
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.,
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- PIV: Conversion of fibrinogen to fibrin is triggered by thrombin.

CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC PIR; E28854; E28854.
DR InterPro; IPR002181; Fibrinogen_C.
DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KM Blood coagulation; Plasma.
FT PEPTIDE 1 9 FIBRINOPEPTIDE B.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1057 MW; DDEE71E9C7267B06 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
DB 6 FH 7

RESULT 11
ANGT BOVIN STANDARD; PRT; 10 AA.
AC P01017;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Angiotensinogen [contains: Angiotensin I (Ang I); Angiotensin II (Ang
DE II); Angiotensin III (Ang III) (Des-Asp[1]-angiotensin II)]
DE (Fragment).
GN AGT OR SERPIN A8.
OS Bos taurus (Bovine).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Buthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
CC Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN 11
RP SEQUENCE.
RA Elliott D.F., Peart W.S.;
RL "The amino acid sequence in a hypertensin.";
RL Biochem. J. 65:246-254(1957).
CC -1- FUNCTION: In response to lowered blood pressure, the enzyme renin
CC cleaves angiotensin I, from angiotensinogen. ACE (angiotensin
CC converting enzyme) then removes a dipeptide to yield the
CC physiologically active peptide angiotensin II, the most potent
CC pressor substance known, which helps regulate volume and mineral
CC balance of body fluids.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- SIMILARITY: Belongs to the serpin family.
DR PIR; A90345; A90345.
DR PDB; 3ERS; 15-JUL-92.
DR InterPro; IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KM Vasconstrictor; Plasma; Serpin; 3D-structure.
FT PEPTIDE 1 10 ANGIOTENSIN I.
FT PEPTIDE 1 10 ANGIOTENSIN II.
FT PEPTIDE 2 8 ANGIOTENSIN III.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1282 MW; CEEFDD761FEDB42 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 FH 3
DB 8 FH 9

RESULT 12
COXM RAT STANDARD; PRT; 10 AA.
ID COXM_RAT

AC P80431.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
 DE (Fragment).
 GN COX7B.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE.

RC STRAIN=Mistar; TISSUE=Liver;
 RX MEDLINE=95324529; PubMed=7601105;
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 RT amino-terminal sequences suggest identity of the fetal heart and the
 RT adult liver isoform";
 RL Eur. J Biochem 230:235-241(1995).
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
 CC chains of cytochrome c oxidase, the terminal oxidase in
 CC mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC PIR: S65387; S65387.
 DR Oxidoreductase; Mitochondrion.
 KW NON TER
 FT 10
 SQ SEQUENCE 10 AA; 1210 MW; CFC70EB71A3326 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FH 3
 ||
 Db 9 FH 10

RESULT 13
 ID PKX_LOCOMI STANDARD; PRT; 10 AA.
 AC P83382;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Periviscerokin (Lom-PVK-1).
 DE Locusta migratoria (Migratory locust).
 OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caellifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_Taxid=7004;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Abdominal periviscerokin organs;
 RX MEDLINE=21896327; PubMed=11897380;
 RA Friedel R., Gaede G.;
 RT "Identification of the abundant neuropeptide from abdominal
 RT periviscerokin organs of locusts";
 RL Peptides 23:621-627(2002).
 CC -1- FUNCTION: Myotropic peptide; increases the frequency of
 CC contraction of the heart and stimulates amplitude and tonus of the
 CC foregut.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1104.5; METHOD=MALDI.
 DR GO: GO:000576; C:extracellular; IDA.
 DR GO: GO:0005184; F:neuropeptide hormone activity; IDA.
 DR GO: GO:0007218; P:neuropeptide signaling pathway; IDA.
 KW Neuropeptide; Amidation.
 FT MOD RES 10
 SQ SEQUENCE 10 AA; 1105 MW; 39811269D6D9C728 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 10;

Best Local Similarity 60.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Oy 1 KPARV 5
 ||
 Db 6 QPFRV 10

RESULT 14
 ID TRPS_LEUMA STANDARD; PRT; 10 AA.
 AC P81740;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tachykinin-related peptide 8 (LemRP 8).
 OS Leucophaea maderae (Maderia cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberidae;
 OC Blaberidae; Leucophaea.
 OX NCBI_Taxid=6988;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Brain;
 RX MEDLINE=97269266; PubMed=9114447;
 RA Wuren J.E., Naessel D.R.;
 RT "Seven tachykinin-related peptides isolated from the brain of the
 RT maderia cockroach; evidence for tissue-specific expression of
 RT isoforms";
 RL Peptides 18:7-15(1997).
 CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
 CC of spontaneous contractions and tonus of hindgut muscle.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Brain.
 CC -1- MASS SPECTROMETRY: MW=1076.9; METHOD=MALDI.
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10
 SQ SEQUENCE 10 AA; 1076 MW; 9E410371B9C87685 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.8e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 2 FH 3
 ||
 Db 6 FH 7

RESULT 15
 ID UKA6_CHLTR STANDARD; PRT; 10 AA.
 AC P38007;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Unknown protein from 2D-page from elementary body (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=813;
 RN [1]
 RP SEQUENCE.

RC STRAIN=L2/434/Bu;
 RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
 RA Comanducci M., Christianen G., Birkelund S., Vreton E., Ratti G.,
 RA Pallini V.;
 RL Submitted (SEP-1994) to Swiss-Prot.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
 DR Sienra-2DPAGE; P38007; -;
 KW NON TER
 FT 10
 SQ SEQUENCE 10 AA; 1243 MW; DAD39A3304B5339 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 5.8e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 FHRVTKD 8
 DB 3 FHRVTKD 9

RESULT 16

COXA_CANFA STANDARD; PRT; 11 AA.

AC P99501;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
 GN COXA.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_Taxid=9615;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
 CC oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.

DR HSC-2DPAGE; P99501; DOG.
 DR InterPro: IPR003204; Cyt_c_oxsa.
 DR Pfam: PF02284; COXA; 1; C_oxsa.
 DR Oxidoreductase; Heme; Mitochondrion; Inner membrane.
 KM NON TER 11
 FT SEQUENCE 11 AA; 1274 MW; 910B35C5B1AB11F5 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 11;
 Best Local Similarity 28.6%; Pred. No. 6.4e+03;
 Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 HRVTKD 9
 DB 5 HETDEEF 11

RESULT 17

EFG_CLOPA STANDARD; PRT; 11 AA.

AC P81350;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Elongation factor G (EF-G) (CP 5) (Fragment).
 GN FUSa.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_Taxid=1501;
 RN [1]
 RP SEQUENCE.

RC STRAIN=WS;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum WS.";
 RL Electrophoresis 19:802-806(1998).

CC -1- FUNCTION: This protein promotes the GTP-dependent translocation of
 CC the nascent protein chain from the A-site to the P-site of the
 CC ribosome.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
 CC EF-G/EF-2 subfamily.
 DR InterPro: IPR00795; EF_GTPbind.
 DR PROSITE: PS00301; EFACITOR_GTP; PARTIAL.
 KM Elongation factor; Protein biosynthesis; GTP-binding.
 FT NON TER 11
 SO SEQUENCE 11 AA; 1337 MW; 412E71F1D9C3B17 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 11;
 Best Local Similarity 40.0%; Pred. No. 6.4e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KFRV 5
 DB 6 KFRV 10

RESULT 18

LICH_BACLI STANDARD; PRT; 12 AA.

AC P82907;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lichenin.
 OS Bacillus licheniformis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_Taxid=1402;
 RN [1]
 RP SEQUENCE.

RC STRAIN=26L-10/3RA;
 RX MEDLINE=21460732; PubMed=11576300;
 RA Pattnaik P., Kaushik J.K., Grover S., Batish V.K.;
 RT "Purification and characterization of a bacteriocin-like compound
 RT (lichenin) produced anaerobically by Bacillus licheniformis isolated
 RT from water buffalo.";
 RL J. Appl. Microbiol. 91:636-645(2001).
 RN [2]
 RP SEQUENCE.

RC STRAIN=26L-10/3RA;
 RA Pattnaik P.;
 RT "Biochemical characterization and molecular genetics of bacteriocin
 RT produced by a selected rumen bacterial isolate.";
 RL Thesis (1999), National Dairy Research Institute / Karnal, India.
 CC -1- FUNCTION: OXYGEN LABILE BACTERIOCIN-LIKE. HAS ANTIBACTERIAL
 CC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC Antibiotic; Bacteriocin.
 KM Antibiocin.
 SO SEQUENCE 12 AA; 1414 MW; 1C059B6CEDA4EB0 CRC64;

Query Match 28.6%; Score 14; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 FH 3
 DB 9 FH 10

RESULT 19

UH03_RAT STANDARD; PRT; 12 AA.

AC P56572;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Unknown protein from 2D-page of heart tissue (Spot P3) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammali; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
ON [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheeler C., Regitz-Zagrosek V., Salikov J.
RA Jungblut P.R.;
RV Submitted (SEP-1998) to Swiss-Prot.
CC -1 MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 8.3, its MW is: 28 kDa.
FT UNSURE 2 2
FT UNSURE 9 9
FT NON_TER 12 12
QX SEQUENCE 12 AA; 1255 MW; 46F58D10DC33053 CRC64;

Query Match	28.6%;	Score 14;	DB 1;	Length 12;
Best Local Similarity	60.0%;	Pred. No. 6.9e+03;		
Matches	3;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY 3 HRVIK 7
|
|
Db 3 HTKIK 7

RESULT	20
XYLA_STRVN	
ID_XYLA_STRVN	STANDARD;
PRT;	12 AA

DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Xylose isomerase (EC 5.3.1.5) (Fragment).
GN XYL.

0C Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales
0C Streptomycetaceae; Streptomyces.
0X NCBI_TaxID=1935;

RN	[1]
RP	SEQUENCE.
RC	STRAIN=LMG 7183;

RX MEDLINE=90104230; PubMed=2604694;
 RA Vangryperre W., Ampe C., Kersters-Hilderson H., Tempst P.;
 RT "Single active-site histidine in D-xylose isomerase from *Streptomyces*

RT mapping.";
RT Biochem. J. 263:195-199(1989).
RL CATALANICA, J. and R. L. B. 1989 = B. 1989

- cc - CALCIUM: Binds 2 magnesium ions per subunit (Potential).
- cc - CALCIUM ACTIVITI: D-Xylose = D-Xylose.
- cc - COFACTOR: Binds 2 magnesium ions per subunit (Potential).
- cc - SUBUNIT: Homotetramer.
- cc - SUBCELLULAR LOCATION: Cytoplasmic

CC -| BOCCELLIDAR LOCATION: cytoplasmic,
CC -| SIMILARITY: Belongs to the xylose isomerase family
DR HAMAP; MF_00455; -; 1.
DR InterPro: IPR001998; Xv]ase_isom

DR PROSITE; PS00172; XYL0SE_ISOMERASE_1; PARTIAL
DR PROSITE; PS00173; XYL0SE_ISOMERASE_2; PARTIAL
KW isomerase; Pentose shunt; Xyl0se metabolism; N

FT	NON_TER	1	1
FT	ACT_SITE	5	5
FT	NON_TER	12	12

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SQ      SEQUENCE      12 AA; 1375 MM; E749268EB1AAAAA1 CRC64;
Query Match      28.6%; Score 14; DB 1; Length 12

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Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	2	FH	3
Db	4	FH	5

RESULT 21

RESULT 21	
BS43_SERPL	
ID_BS43_SERPL	STANDARD; PRT; 9 AA

AC P83375; DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin serracin P 43 kDa subunit (Fragment).
OS *Serratia plymuthica*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
OC Enterobacteriaceae; Serratia.
OX NCBI_TaxID=82996;

RN [1]
RP SEQUENCE, AND FUNCTION.
RC STRAIN=J7;
RX MEDLINE=22293561; Pubmed=12406768;

RA Jabrane A., Sabri A., Compere P., Jacques P., Vandenberghe I.,
 RA Van Beumen J., Thonart P.,
 RT "Characterization of serracin P, a phage-tail-like bacteriocin, and

CC -1- FUNCTION: Major component of a prophage tail sheath (Probable).
CC ENVIRONMENT: Antibacterial activity against Gram-negative bacteria.

CC	- FUNCTION; Antibacter
CC	E.amylovora.
KW	Antibiotic; Bacteriocin
FT	NON TEP ^a

E1		9	AA;	1095	MW;	1E66D412C871E1FB	CRC64
SQ	SEQUENCE						
Query Match				26.5%	Score 13:	DB 1:	Leno

Query Match	26.5%	Score 13	DB 1	Length 9
Best Local Similarity	16.7%	Pred. No.	1.4e+05	
Matches	1	Conservative	3	Mismatches 2
				Indels 0
				Gaps 0

QY	2	FHRVIK	7
	:	:	:
Db	2	YHGGVR	7

RESULT 22	
D1_NEPNO	STANDARD;
ID_ D1_NEPNO	PRT; 9 AA

AC	P24816;
DT	01-MAR-1992 (Rel. 21, Created
DT	01-MAR-1992 (Rel. 21, Last se

DT 01-MAR-1992 (Rel. 21, last annotation update
DE Gastrin/cholecystokinin-like peptide D1.
OS Nephrops norvegicus (Norway lobster).

0C Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
0C Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
0C Nephropoidea; Nephropidae; Nephrops.

OA NCBI_taxid=6829;
 RN [1]
 RP SEQUENCE.
 RC TRS-Start:
 PC

RC MEDLINE=92082847; PubMed=1747388;
RX Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;
BT "Structure and biological activity of crustacean gastrointestinal

CC -1- FUNCTION: May control digestion processes in crustaceans.
 RL Biochemle 73:1233-1239(1991).

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family
DR PIR; S47432; S47432.
KW Hormone.

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SQ      SEQUENCE      9 AA;      1038 MW;      60EC79CAB6D8787B CRC64
Query Match      26.5%;      Score 13;      DB 1;      Length 1038

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Best Local Similarity: 66.7%; Pred. No. 1.4e+05;
Matches: 2; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY	7	KDF	9
	:		
Db	5	QDF	7

RESULT 23

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RESULT 23
PAR1 CALVO
ID _PAR1_CALVO STANDARD; PRT; 9 AA

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AC P41856;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 1.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroides;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Rehfeld J.F., Thorpe A., Sewell J.C., Scott A.G., Orchard I.,
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FMRP (FMRamide related peptide)
family.
CC PIR; A41978; A41978.
DR Neuropetide; Amidation.
KW MOD RES
FT MOD RES
SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB6C6C7 CRC64;
Query Match 26.5%; Score 13; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 7 KDF 9
DB 4 QDF 6
RESULT 24
FMR2 CALVO STANDARD; PRT; 9 AA.
ID FMR2 CALVO
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroides;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Rehfeld J.F., Thorpe A., Sewell J.C., Scott A.G., Orchard I.,
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FMRP (FMRamide related peptide)
family.
CC PIR; B41978; B41978.
DR Neuropetide; Amidation.
KW MOD RES
FT MOD RES
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB6C5A7 CRC64;
Query Match 26.5%; Score 13; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 KDF 9
DB 4 QDF 6
RESULT 25
FMR3 CALVO STANDARD; PRT; 9 AA.
ID FMR3 CALVO
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroides;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Rehfeld J.F., Thorpe A., Sewell J.C., Scott A.G., Orchard I.,
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FMRP (FMRamide related peptide)
family.
CC PIR; C41978; C41978.
DR Neuropetide; Amidation.
KW MOD RES
FT MOD RES
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;
Query Match 26.5%; Score 13; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 7 KDF 9
DB 4 QDF 6
RESULT 26
FMR4 CALVO STANDARD; PRT; 9 AA.
ID FMR4 CALVO
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroides;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Rehfeld J.F., Thorpe A., Sewell J.C., Scott A.G., Orchard I.,
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the FMRP (FMRamide related peptide)
family.
CC PIR; D41978; D41978.

KW Neuropeptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB6D457 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDF 9
 :||
 4 QDF 6

Db

RESULT 27
 FAR5_CALVO STANDARD; PRT; 9 AA.
 ID FAR5_CALVO
 AC P41860;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRamide 5.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Calliphoridae; Calliphora.
 NCBI_TaxID=27454;

RN NCBI_TaxID=27454;
 RN SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Rehfeld J.F., Thorpe A.; Scott A.G., Orchard I.,
 "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 neuropeptides (designated calliFMRamides) from the blowfly
 Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 family.
 DR PIR; E41978; E41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1068 MW; 39D10699CAB6D867 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDF 9
 :||
 4 QDF 6

Db

RESULT 28
 FAR6_CALVO STANDARD; PRT; 9 AA.
 ID FAR6_CALVO
 AC P41861;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRamide 6.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Calliphoridae; Calliphora.
 NCBI_TaxID=27454;

RN NCBI_TaxID=27454;
 RN SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 Rehfeld J.F., Thorpe A.;
 "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 neuropeptides (designated calliFMRamides) from the blowfly
 neuropeptides (designated calliFMRamides) from the blowfly

RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 family.
 DR PIR; E41978; E41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1058 MW; 96D10699CAB6D865 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDF 9
 :||
 4 QDF 6

Db

RESULT 29
 FAR7_CALVO STANDARD; PRT; 9 AA.
 ID FAR7_CALVO
 AC P41862;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRamide 7.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Calliphoridae; Calliphora.
 NCBI_TaxID=27454;

RN NCBI_TaxID=27454;
 RN SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 Rehfeld J.F., Thorpe A.;
 "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 neuropeptides (designated calliFMRamides) from the blowfly
 Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 family.
 DR PIR; G41978; G41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1081 MW; E1D10699CAB6D86A CRC64;

Query Match 26.5%; Score 13; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDF 9
 :||
 4 QDF 6

Db

RESULT 30
 FAR1_SARBU STANDARD; PRT; 9 AA.
 ID FAR1_SARBU
 AC P83350;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FMRamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Sarcophagidae; Sarcophaga.
 NCBI_TaxID=7385;

RN NCBI_TaxID=7385;
 RN SEQUENCE.
 RC TISSUE=CNS;
 AND FUNCTION.

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RX MEDLINE=22342733; PubMed=12438685;
RA Weensen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
RA Nachman R.J., Huybrechts R., De loof A., Schoofs L.;
RT "Identification in Drosophila melanogaster of the invertebrate G
RT protein-coupled FMRFamide receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
CC -!- FUNCTION: Has modulatory actions at skeletal neuromuscular
CC junctions.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the FMRP (FMRFamide related peptide)
CC family.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDF 9
Db 4 QDF 6

RESULT 31
MALE_KLEBN STANDARD; PRT; 10 AA.
AC Q05564.
BT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Maltose-binding periplasmic protein (Maltodextrin-binding protein)
DE (MBP) (Fragment).
GN MALE.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.
OX NCBI_TaxID=573;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1033-SP14 / KAY2026;
RX MEDLINE=93211295; PubMed=8459773;
RA Bachelier S., Perrin D., Holnung M., Gilson E.;
RT "Bacterial interspersed mosaic elements (BIMEs) are present in the
RT genome of Klebsiella."
RL Mol. Microbiol. 7:537-544(1993).
CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CC CHEMOTAXIS TOWARD MALTOOLIGOSACCHARIDES.
CC -!- SUBCELLULAR LOCATION: Periplasmic.
CC -!- SIMILARITY: Belongs to the bacterial extracellular solute-binding
CC protein family 1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X68329; CAA48406.1; -
DR InterPro; IPR006061; SBP_dgml.
DR PROSITE; PS01037; SBP_BACTERIAL_1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDA CRC64;

Query Match 26.5%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 6 IKD 8
Db 1 LKD 3

RESULT 32
TKNI_SCYCA STANDARD; PRT; 10 AA.
ID TKNI_SCYCA
AC P08608.
BT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Scyliorhinin I.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=86192829; PubMed=2422058;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyliorhinin I and II: two novel tachykinins from dogfish gut.";
RL FEBS Lett. 200:111-116(1986).
RN [2]
RP SEQUENCE.
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secreteagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the tachykinin family.
CC PIR; A24867; A24867.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1219 MW; D0602D6B59C3A9A9 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFH 3
Db 5 KEY 7

RESULT 33
TKNB_ONCMY STANDARD; PRT; 10 AA.
ID TKNB_ONCMY
AC P28500.
BT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neurokinin A (Substance K) (Neurokinin I).
OS Onchorynchus mykiss (Rainbow trout) (Salmo gairdneri), and
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Percaractopterygii; Salmoniformes; Salmonidae; Onchorynchus.
OX NCBI_TaxID=8022; 8049;
RN [1]
RP SEQUENCE.
RC SPECIES=O. mykiss, and G. morhua;
RC TISSUE=Brain;

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RX MEDLINE=92228992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
of the cod and trout."
RL Bur. U. Biochem. 206:659-664(1992).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
CC evoke behavioral responses, are potent vasodilators and
CC secretagogues, and contract (directly or indirectly) many smooth
CC muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR: S23186; S23186.
DR PIR: S23307; S23307.
DR InterPro: IPR002040; Tachy Neurokinin.
DR Pfam: PF02202; Tachykinin; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; 13684062C95B440 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 9e+03;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRV 5
DB 1 HKI 3

RESULT 34
TKS1_AEDAE STANDARD; PRT; 10 AA.
AC P42634;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialokinin I.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxID=7159;

RN (1)
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
mosquito Aedes aegypti."
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -1- FUNCTION: Vasodilatory peptide. May activate macrophages at the
CC site of feeding.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR InterPro: IPR002040; Tachy Neurokinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1145 MW; 3DCFB6B59C33A8 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFH 3
DB 5 KFY 7

RESULT 35
TKS2_AEDAE STANDARD; PRT; 10 AA.
ID TKS2_AEDAE
AC P42635;

DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialokinin II.
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.
OX NCBI_TaxID=7159;

RN (1)
RC STRAIN=Rockefeller; TISSUE=Salivary gland;
RX MEDLINE=94105119; PubMed=8278354;
RA Champagne D.E., Ribeiro J.M.C.;
RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
mosquito Aedes aegypti."
RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
CC -1- FUNCTION: Vasodilatory peptide. May activate macrophages at the
CC site of feeding.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR: B49581; B49581.
DR InterPro: IPR002040; Tachy Neurokinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1146 MW; 3DC77C6B59C33A8 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFH 3
DB 5 KFY 7

RESULT 36
XYNB_DICB4 STANDARD; PRT; 10 AA.
ID XYNB_DICB4
AC P80717;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Endo-1,4-beta-xylanase B (EC 3.2.1.8) (Xylanase B)
DE (1,4-beta-D-xylan xylanohydrolase B) (Fragmant).
OS Dictyoglomus sp. (strain B4A).
OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
OX NCBI_TaxID=69007;

RN (1)
RC STRAIN=Adamsen A.K., Jacobsen S., Ahring B.K.;
RT Submitted (OCT-1996) to Swiss-Prot.
CC -1- CATALYTIC ACTIVITY: Endomonoxyolysis of 1,4-beta-D-xylosidic
CC linkages in xylyans.
CC -1- PATHWAY: Xylan degradation.
CC -1- SIMILARITY: Belongs to cellulase family F (family 10 of glycosyl
CC hydrolases).
DR InterPro: IPR001000; Glyco hydro 10.
DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; PARTIAL.
KW Xylan degradation; Hydrolase; Glycosidase.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA; 1144 MW; 4554322AA72041A3 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 IKD 8
DB 8 LKD 10

RESULT 37

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CSIS_BACSU
ID CSIS_BACSU STANDARD; PRT; 11 AA.
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CSIS (11 kDa cold shock protein) (Fragment).
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
RX MEDLINE=96345629; PubMed=8755892;
RA Gramann P.L., Schmid R., Marahiel M.A.;
RL Submitted (OCT-1997) to Swiss-Prot.
RN [2]
RP CHARACTERIZATION.
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Gramann P., Schroeder K., Schmid R., Marahiel M.A.;
RL "Cold shock, stress-induced proteins in Bacillus subtilis.";
RN [2]
RP Bacteriol. 178:4611-4619(1996).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- INDUCTION: In response to low temperature.
CC -1- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON TER 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6FCBE6322C330 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KDF 9
DB 6 VKPF 9

RESULT 38
NM NM CANFA STANDARD; PRT; 11 AA.
ID NM CANFA STANDARD; PRT; 11 AA.
AC P49820;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-OCT-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE (EC 1.6.99.3) (Fragment).
GN NDUFV2.
OS Caris familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163140; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RL "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RT Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
FRAGMENT OF THE ENZYME.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC -1- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC -1- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
mitochondrial inner membrane.
OS -1- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR HSC-2DPAGE; P49820; DOG;
DR InterPro; IPR002023; Cmp1x1_24kDa.
DR PROSITE; PS01099; COMPLEX1_24K; PARTIAL.

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KM Oxidoreductase; NAD, Ubiquinone; Mitochondrion; Metal-binding;
KM Iron-sulfur; Iron; 2Fe-2S.
FT NON TER 11
SQ SEQUENCE 11 AA; 1099 MW; 267F5369C9C72D2D8 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HR 4
DB 9 HR 10

RESULT 39
NM NM PHYFU STANDARD; PRT; 11 AA.
ID NM PHYFU STANDARD; PRT; 11 AA.
AC P08615;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Physalaemin.
OS Physalaemus fuscumaculatus (Neotropical frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Leptodactylidae;
OC Leptodactylinae; Physalaemus.
OC NCBI_TaxID=8378;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=6607612; PubMed=5857249;
RA Espamer V., Anastasi A., Bertaccini G., Cel J.M.;
RL "Structure and pharmacological actions of physalaemin, the main
RT active polypeptide of the skin of Physalaemus fuscumaculatus.";
RL Experientia 20:489-490(1964).
CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
evoked behavioral responses, are potent vasodilators and
secretagogues, and contract (directly or indirectly) many smooth
muscles.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the tachykinin family.
DR PIR; S07201; S07201.
DR InterPro; IPR002040; Tachy_Neurokinin.
DR Pfam; PF02202; Tachykinin; 1.
DR PROSITE; PS00267; TACHYKININ; 1.
KM Amphibian defense peptide; Tachykinin; Neuropeptide; Amidation;
KM Pyroliidone carboxylic acid.
FT MOD_RES 11
FT MOD_RES 11
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1283 MW; 3293693B59C33457 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 9.9e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KFH 3
DB 6 KVF 8

RESULT 40
NM RFL_CONSP STANDARD; PRT; 12 AA.
ID RFL_CONSP STANDARD; PRT; 12 AA.
AC F58805;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conorfamide-Srl.
OS Conus spurius (Alphabet cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.

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OX NCB1_TaxID=192919;
RN (1)
RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=21605839; PubMed=11738233;
RA Mallo M., Aguilar M.B., Lopez-Vera E., Craig A.G., Bulaj G.,
RA Olivera B.M., Heimer de la Cereza E.P.;
RT "Conoramide, a Conus venom peptide belonging to the Rfamamide family of
RT neuropeptides."
RL Toxicol 40:401-407(2002).
CC -1- FUNCTION: Causes hyperactivity in mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1454.8; METHOD=Electrospray.
CC -1- SIMILARITY: Belongs to the Rfap (Rfamamide related peptide)
CC family.
KM Neurotoxin; Toxin; Amidation.
FT MOD RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1456 MW; 2510671B49D772D3 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 FHRV 4
DB 9 FRI 11

RESULT 41
NP4_LYMST STANDARD; PRT; 13 AA.
ID NP4_LYMST
AC P80181;
DT 01-JUL-1993 (Rel. 26, Last Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 4.
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCB1_TaxID=6523;
RN (1)
RN SEQUENCE.
RP TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates";
RL Eur. J. Biochem. 213:875-879(1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
DR PIR: S32474; S32474.
KW Neuropeptide; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1503 MW; 9CA07BBB56D5B455 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRV 5
DB 2 FRI 5

RESULT 42
NP5_LYMST STANDARD; PRT; 13 AA.
ID NP5_LYMST
AC P80182;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea-Df-amide 5.

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OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
OC Lymnaeidae; Lymnaeidae; Lymnaea.
OX NCB1_TaxID=6523;
RN (1)
RN SEQUENCE.
RP TISSUE=Ganglion;
RX MEDLINE=93238777; PubMed=8477756;
RA Johnson A.H., Rehfeld J.F.;
RT "Lymnaea stagnalis, a new family of neuropeptides from the pond snail,
RT Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates";
RL Eur. J. Biochem. 213:875-879(1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
DR PIR: S32475; S32475.
KW Neuropeptide; Amidation.
FT MOD RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1476 MW; 9CA07BBB56D5A5A5 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FHRV 5
DB 2 FRI 5

RESULT 43
PHGR_EUBOX STANDARD; PRT; 13 AA.
ID PHGR_EUBOX
AC P57793;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phloroglucinol reductase (EC 1.3.1.57) (Fragment).
OS Eubacterium oxidoreducens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Eubacteriaceae;
OC Eubacterium.
OX NCB1_TaxID=1732;
RN (1)
RN SEQUENCE AND CHARACTERIZATION.
RP STRAIN=G-41;
RX MEDLINE=89174692; PubMed=2925649;
RA Haddock J.D., Perry J.G.;
RT "Purification and properties of phloroglucinol reductase from
RT Eubacterium oxidoreducens G-41."
RL J. Biol. Chem. 264:4423-4427(1989).
CC -1- FUNCTION: FUNCTIONS IN THE PATHWAY OF ANAEROBIC DEGRADATION OF
CC TRIMETHOXYBENZENES BY CATALYZING REDUCTION OF THE AROMATIC NUCLEUS
CC PRIOR TO RING FISSION.
CC -1- CATALYTIC ACTIVITY: Dihydrophloroglucinol + NADP(+) =
CC phloroglucinol + NADPH.
CC -1- SUBUNIT: Homodimer.
CC -1- MISCELLANEOUS: TEMPERATURE AND PH OPTIMA ARE 40 DEGREES CELSIUS
CC AND 7.8 IN THE FORWARD DIRECTION.
DR PIR: A32453; A32453.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; NADP.
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1527 MW; 427E2E0833F1CB13 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDF 9
DB 6 KDF 8

RESULT 44
SA2A_ONCMY STANDARD; PRT; 13 AA.
ID SA2A_ONCMY

```

AC P82238;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Salmocidin 2A (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Serum;
 RA Henry M.A., Secombes C.J.;
 RT "Purification and partial characterization of antibacterial peptides
 from rainbow trout, *Oncorhynchus mykiss*.";
 RL Submitted (DEC-1999) to Swiss-Prot
 CC -!- FUNCTION: Antibacterial activity against Gram-negative bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma serum.
 KW Antibiotic.
 KW NON TER
 FT 13
 SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AF6C45873 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 13;
 Best Local Similarity 40.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 VIKDF 9
 | : | :
 Db 4 VLKGY 8

RESULT 45
 SA2B_ONCMY STANDARD; PRT; 13 AA.
 ID SA2B_ONCMY
 AC P82239;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Salmocidin 2B (Fragment).
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Serum;
 RA Henry M.A., Secombes C.J.;
 RT "Purification and partial characterization of antibacterial peptides
 from rainbow trout, *Oncorhynchus mykiss*.";
 RL Submitted (DEC-1999) to Swiss-Prot.
 CC -!- FUNCTION: Antibacterial activity against Gram-negative bacteria.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Plasma serum.
 KW Antibiotic.
 KW NON TER
 FT 13
 SQ SEQUENCE 13 AA; 1400 MW; 5FFB792AF6B5873 CRC64;

Query Match 26.5%; Score 13; DB 1; Length 13;
 Best Local Similarity 40.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 VIKDF 9
 | : | :
 Db 4 VLKGY 8

Search completed: August 30, 2004, 10:50:16
 Job time : 3.55068 secs

GenCore version 5.1.6.
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 8.66554 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469a-2

Perfect score: 50

Sequence: 1 DFMIQGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_proteint:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	44.0	10	13	Q8UWV2
2	22	44.0	12	4	Q9H3W2
3	22	44.0	12	13	Q8UWV0
4	22	44.0	12	13	Q8UWV8
5	22	44.0	13	9	Q8HA05
6	20	40.0	12	4	Q13865
7	18	36.0	8	6	Q9T778
8	18	36.0	9	13	Q9P568
9	18	36.0	10	2	Q51812
10	18	36.0	10	6	Q95NB1
11	18	36.0	11	2	Q87882
12	18	36.0	11	6	Q95J20
13	18	36.0	11	6	Q95NB6
14	18	36.0	11	6	Q95U19
15	18	36.0	12	2	Q46712
16	18	36.0	12	6	Q9N2B9

17	18	36.0	12	6	Q95NB3	Q95nb3 eulemur ful
18	18	36.0	12	6	Q9N2B8	Q9n2b8 pongo pygma
19	18	36.0	12	6	Q9N2C0	Q9n2c0 pan troglod
20	18	36.0	13	6	Q95NB7	Q95nb7 eulemur ful
21	18	36.0	13	15	Q98YJ7	Q98yj7 human immun
22	17	34.0	8	13	Q15902	Q15902 homo sapien
23	17	34.0	8	13	Q90ZV5	Q90zv5 fulica leuc
24	17	34.0	10	4	Q96Q47	Q96q47 homo sapien
25	17	34.0	11	2	Q47420	Q47420 escherichia
26	17	34.0	12	4	Q9H1Z6	Q9h1z6 homo sapien
27	17	34.0	13	7	Q19690	Q19690 homo sapien
28	16	32.0	9	10	Q863C6	Q863c6 glycine max
29	16	32.0	10	4	Q725A2	Q725a2 homo sapien
30	16	32.0	12	2	Q542Z6	Q542z6 saccharopol
31	16	32.0	12	4	Q726W4	Q726w4 homo sapien
32	16	32.0	12	6	Q46664	Q46664 macropus ro
33	16	32.0	12	10	Q02320	Q02320 pinus sylve
34	16	32.0	12	10	Q38715	Q38715 atachis hyp
35	16	32.0	13	3	Q93824	Q93824 candida tro
36	16	32.0	13	10	Q93980	Q93980 brassica ol
37	16	32.0	14	10	Q814P5	Q814p5 zea mays (m
38	16	32.0	14	12	Q86578	Q86578 sigma virus
39	16	32.0	14	15	Q88400	Q88400 simian t-ly
40	16	32.0	14	15	Q8UT17	Q8ut17 human immun
41	15	30.0	8	4	Q9P0K3	Q9p0k3 homo sapien
42	15	30.0	9	4	Q9BQT4	Q9bqt4 homo sapien
43	15	30.0	9	13	Q92009	Q92009 gallus gall
44	15	30.0	11	3	Q9H2N8	Q9h2n8 candida rug
45	15	30.0	11	7	Q78786	Q78786 oreochromis

ALIGNMENTS

RESULT 1	Q8UWV2	PRELIMINARY;	PRT;	10 AA.
AC	Q8UWV2;			
DT	01-MAR-2002 (TREMBL:rel. 20, Created)			
DT	01-MAR-2002 (TREMBL:rel. 20, Last sequence update)			
DT	01-JUN-2003 (TREMBL:rel. 24, Last annotation update)			
DE	AMPA receptor subunit 2 alpha (Fragment).			
GN	GLUR2A.			
OS	Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;			
OC	Cichlidae; Oreochromis.			
OX	NCBI_TaxID=8127;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kung S.-S., Chen C.-C., Chen Y.-C., Chen B.-Y., Lin W.-H., Chow W.-Y.;			
RT	"O/R RNA editing of the AMPA receptor subunit GLUR2 transcript evolves			
RT	no later than the appearance of cartilaginous fishes."			
RU	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF550050; AAD57192.1; -			
DR	GO; GO:0004872; F:receptor activity; IEA.			
KM	Receptor.			
FT	NON_TER	1	1	
FT	NON_TER	10	10	
SQ	SEQUENCE	10 AA;	1153 MW;	721A6F5AAB666C4 CRC64;
Qy	Query Match	Score 22;	DB 13;	Length 10;
Db	Best Local Similarity	71.4%;	Pred. No. 1.3e+03;	
	Matches	5;	Conservative	0;
			Mismatches	2;
			Indels	0;
			Gaps	0;
RESULT 2	Q9H3W2	2 DFMIQGD 8		
		1 FMIQGD 7		

ID Q8H3W2 PRELIMINARY; PRT; 12 AA.
 AC Q8H3W2;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE TRE17 protein.
 GN TRE17 GENE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94010310; PubMed=8406013;
 RA Ono M., Nakamura T., Hillova J., Hill M.;
 RT "Identification of novel sequences in the repertoire of hypervariable
 RT TRE17 genes from immortalized nonmalignant and malignant human
 RT keratinocytes.";
 RL Gene 131:209-215(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93228825; PubMed=8471161;
 RA Ono M., Nakamura T., Mariage-Samson R., Hillova J., Hill M.;
 RT "Human TRE17 oncogene is generated from a family of homologous
 RT polymorphic sequences by single-base changes.";
 RL DNA Cell Biol. 12:107-118(1993).
 DR EMBL; X71371; CAC16150.1; -
 SQ SEQUENCE 12 AA; 1252 MW; 6E17AFDE83AD87B CRC64;

Query Match 44.0%; Score 22; DB 4; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGCD 8
 DB 3 MVEGAD 8

RESULT 3
 Q8UVW0 PRELIMINARY; PRT; 12 AA.
 AC Q8UVW0;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE AMPA receptor subunit 2 (Fragment).
 GN GLUR2.
 OS Rana catesbeiana (Bull Frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OK NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kung S.-S., Chen C.-C., Chen Y.-C., Chen B.-Y., Lin W.-H., Chow W.-Y.;
 RT "Q/R RNA editing of the AMPA receptor subunit Glur2 transcript evolves
 RT no later than the appearance of cartilaginous fishes.";
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF350052; AAL57194.1; -
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1269 MW; DD1A28D235B86C6 CRC64;

Query Match 44.0%; Score 22; DB 13; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGCD 8
 DB 3 FMIOGCD 9

RESULT 4
 Q8UV8 PRELIMINARY; PRT; 12 AA.
 AC Q8UV8;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE AMPA receptor subunit 2 (Fragment).
 GN GLUR2.
 OS Squalus acanthias (Spiny dogfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Squaloidei; Squalidae; Squalus.
 OK NCBI_TaxID=7797;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kung S.-S., Chen C.-C., Chen Y.-C., Chen B.-Y., Lin W.-H., Chow W.-Y.;
 RT "Q/R RNA editing of the AMPA receptor subunit Glur2 transcript evolves
 RT no later than the appearance of cartilaginous fishes.";
 RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF350054; AAL57196.1; -
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1253 MW; DD1A3E0835B86C6 CRC64;

Query Match 44.0%; Score 22; DB 13; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.6e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGCD 8
 DB 3 FMIOGCD 9

RESULT 5
 Q8HA05 PRELIMINARY; PRT; 13 AA.
 AC Q8HA05;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Bacteriophage Iahm1.
 OC Viruses.
 OK NCBI_TaxID=173830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA El-Sayed A.A.A., Wielek L.H., Baljer G., Stamm I., Kroeger M.;
 RT "Identification of Shiga toxin producing prophages in E.coli from
 RT bovine reveal new insights into toxic phage evolution.";
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA El-Sayed A.A.A.;
 RT "Molecular characterisation of two shiga toxin encoding bacteriophages
 RT from enterohaemorrhagic Escherichia coli.";
 RL Thesis (2000), Department of Veterinary Medicine.
 DR EMBL; AF413275; CAC95073.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 13 AA; 1378 MW; 3F479FA753821878 CRC64;

Query Match 44.0%; Score 22; DB 9; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 IOGCD 8
 DB 4 VOQGE 8

RESULT 6
 Q13865

ID 013865 PRELIMINARY; PRT; 12 AA.
 AC 013865;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Kinesin light chain.
 GN BETA-KINESIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=97101110; PubMed=8945637;
 RA Chernajovsky Y., Brown A., Jones T.A.;
 RT "Promoter first exon/intron characterization and chromosomal location
 of the human light chain (beta) Kinesin gene."
 RL DNA Cell Biol. 15:965-974 (1996).
 DR EMBL; X69658; CAA49349.1; -.
 DR PIR; S43170; S43170.
 SQ SEQUENCE 12 AA; 1274 MW; 3FB8D34FE165A5B8 CRC64;

Query Match 40.0%; Score 20; DB 4; Length 12;
 Best Local Similarity 60.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 MIOGG 7
 ||:|
 DB 1 MIOGG 5

RESULT 7

ID 09TT78 PRELIMINARY; PRT; 8 AA.
 AC 09TT78;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Thymidylate synthase (Fragment).
 GN TS.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015404; PubMed=11130975;
 RA Brouillette J.A., Andrew J.R., Venta P.J.;
 RT "Estimate of nucleotide diversity in dogs with a pool-and-sequence
 method."
 RL Mamm. Genome 11:1079-1086 (2000).
 DR EMBL; AF202073; AAF20918.1; -.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 8 AA; 899 MW; 6731A1E059CA867 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GDF 9
 |||
 DB 2 GDF 4

RESULT 8

ID 09PS68 PRELIMINARY; PRT; 9 AA.
 AC 09PS68;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE low density lipoprotein receptor-related protein (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=2011685; PubMed=1918027;
 RA Stifani S., Barber D.V., Aebbersold R., Steyrer E., Shen X., Nimpf J.,
 RA Schneider W.J.;
 RT "The laying hen expresses two different low density lipoprotein
 receptor-related proteins."
 RL J. Biol. Chem. 266:19079-19087 (1991).
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 9 AA; 1039 MW; 895EC68B5AB2CDC1 CRC64;

Query Match 36.0%; Score 18; DB 13; Length 9;
 Best Local Similarity 40.0%; Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFMIO 5
 ||:|
 DB 5 DFMIO 9

RESULT 9

ID 051812 PRELIMINARY; PRT; 10 AA.
 AC 051812;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE DNA helicase (Fragment).
 GN TRAI.
 OS Escherichia coli.
 OG Plasmid F.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K-12;
 RX MEDLINE=92009201; PubMed=1916281;
 RA Cram D.S., Loh S.M., Cheah K.C., Skurray R.A.;
 RT "Sequence and conservation of genes at the distal end of the transfer
 RT region on plasmids F and R6-5."
 RL Gene 104:85-90 (1991).
 DR EMBL; M38047; AAA98090.1; -.
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0004386; F:helicase activity; IEA.
 KW Helicase; Plasmid.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA; 1088 MW; 59A3047731A3B13 CRC64;

Query Match 36.0%; Score 18; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GGD 8
 |||
 DB 8 GGD 10

RESULT 10

ID 09SNB1 PRELIMINARY; PRT; 10 AA.
 AC 09SNB1;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Malic enzyme (Fragment).

OS Eulemur fulvus (brown lemur).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Strepsirhini; Lemnidae; Eulemur.
 OX NCBI_TaxID=13515;

RA "A genetic assessment of a red-fronted/white-collared lemur hybrid
 RT zone at Andringitra, Madagascar."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF258167; AAK53147.1; -
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1075 MW; DD492E66D9D2C9D2 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 10;
 Best Local Similarity 60.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIOG 6
 DB 4 FVFOG 8

RESULT 11

AC 087882 PRELIMINARY; PRT; 11 AA.
 AC 087882;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE ALKYL hydroperoxide reductase (Fragment).
 GN AHPC.
 OS Mycobacterium xenopi.
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1789;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC19250;
 RX MEDLINE=98406038; PubMed=9733688;
 RA Pagan-Ramos E., Song J., McFalone M., Mudd M.H., Deric V.;
 RT "Oxidative stress response and characterization of the oxyr-ahpc and
 furA-katG loci in Mycobacterium marinum."
 RL J. Bacteriol. 180:4856-4864 (1998).
 DR EMBL; U43810; AAC61663.1; -
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1147 MW; 45458CBI787041A7 CRC64;

Query Match 36.0%; Score 18; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 GGGF 9
 DB 7 GGGF 10

RESULT 12

AC 095J20 PRELIMINARY; PRT; 11 AA.
 AC 095J20;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Malic enzyme (Fragment).
 OS Eulemur fulvus albocollaris.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Strepsirhini; Lemnidae; Eulemur.
 OX NCBI_TaxID=122224;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wyner Y.M., Johnson S.E., Desalle R.;

RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
 RT zone at Andringitra, Madagascar."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF258173; AAK53128.1; -
 DR EMBL; AF258145; AAK53125.1; -
 DR EMBL; AF258147; AAK53127.1; -
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1204 MW; C7CD492E66D9D2C9 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIOG 6
 DB 4 FVFOG 8

RESULT 13

AC 095NB6 PRELIMINARY; PRT; 11 AA.
 AC 095NB6;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Malic enzyme (Fragment).
 OS Eulemur fulvus rufus.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Strepsirhini; Lemnidae; Eulemur.
 OX NCBI_TaxID=47179;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wyner Y.M., Johnson S.E., Desalle R.;
 RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
 RT zone at Andringitra, Madagascar."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF258149; AAK53128.1; -
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1204 MW; C7CD492E66D9D2C9 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 11;
 Best Local Similarity 60.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIOG 6
 DB 4 FVFOG 8

RESULT 14

AC 095J19 PRELIMINARY; PRT; 11 AA.
 AC 095J19;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Malic enzyme (Fragment).
 OS Eulemur fulvus (brown lemur).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euthera; Primates; Strepsirhini; Lemnidae; Eulemur.
 OX NCBI_TaxID=13515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wyner Y.M., Johnson S.E., Desalle R.;
 RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
 RT zone at Andringitra, Madagascar."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF258170; AAK53150.1; -
 DR EMBL; AF258173; AAK53151.1; -
 DR EMBL; AF258173; AAK53153.1; -

DR EMBL; AF258175; AAK53155.1; -
 DR EMBL; AF258178; AAK53158.1; -
 DR EMBL; AF258179; AAK53159.1; -
 DR EMBL; AF258181; AAK53161.1; -
 DR EMBL; AF258182; AAK53162.1; -
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 11 AA, 1204 MW; C7CD492E6D9D2C9 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 12;
 Best Local Similarity 60.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOG 6
 Db 4 FVFOJ 8

RESULT 15
 ID Q46712 PRELIMINARY; PRT; 12 AA.
 AC Q46712.
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Escherichia coli.
 OG Plasmid R100.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86250614; PubMed=3522549;
 RA Fee B.E., Dempsey W.B.;
 RT "Cloning, mapping, and sequencing of plasmid R100 tram and fmp
 RT genes";
 RL J. Bacteriol. 167:336-345(1986).
 DR EMBL; M13054; AAA8503.1; -
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 12 AA, 1295 MW; 640674B567A775A4 CRC64;

Query Match 36.0%; Score 18; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GDF 9
 Db 10 GDF 12

RESULT 16
 ID Q9N2B9 PRELIMINARY; PRT; 12 AA.
 AC Q9N2B9.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Indolethylamine N-methyltransferase (Fragment).
 GN INMT.
 OS Gorilla gorilla (Gorilla).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=gorilla-UI;
 RA Kitano T., Kobayakawa H., Saitou N.;
 RT "Silver Project";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB041364; BAA94453.1; -
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 GO; GO:0008168; F:methyltransferase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.
 KW Methyltransferase; Transferase.
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 12;
 Best Local Similarity 100.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
 Db 7 GGD 9

RESULT 17
 ID Q95NB3 PRELIMINARY; PRT; 12 AA.
 AC Q95NB3.
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Malic enzyme (Fragment).
 OS Eulemur fulvus (brown lemur).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.
 OX NCBI_TaxID=13515;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wyner Y.M., Johnson S.E., Desalle R.;
 RT "A genetic assessment of a red-fronted/white-collared lemur hybrid
 RT zone at Andringitra, Madagascar";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF258164; AAK53144.1; -
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 12 AA, 1275 MW; D547CD492E6D9D2 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 12;
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOG 6
 Db 4 FVFOJ 8

RESULT 18
 ID Q9N2B8 PRELIMINARY; PRT; 12 AA.
 AC Q9N2B8.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Indolethylamine N-methyltransferase (Fragment).
 GN INMT.
 OS Pongo pygmaeus (Orangutan).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pongo.
 OX NCBI_TaxID=9600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=oran-P013;
 RA Kitano T., Kobayakawa H., Saitou N.;
 RT "Silver Project";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB041365; BAA94454.1; -
 DR GO; GO:0008168; F:methyltransferase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 KW Methyltransferase; Transferase.
 FT NON TER 12
 FT NON TER 12
 SQ SEQUENCE 12 AA, 1290 MW; CF079554917861A9 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
DB 7 GGD 9

RESULT 19

Q9N2C0 PRELIMINARY; PRT; 12 AA.
AC Q9N2C0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN INMT.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
RX NCBI_Taxid=9598;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=chmp-220;
RA Kitano T., Kobayakawa H., Saitou N.;
RT "Silver Project."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041363; BAA94452.1; -
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1289 MM; CF0798B2917861A9 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
DB 7 GGD 9

RESULT 20

Q95NB7 PRELIMINARY; PRT; 13 AA.
AC Q95NB7;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Malic enzyme (Fragment).
OS Eulemur fulvus albocollaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirhini; Lemnidae; Eulemur.
RX NCBI_Taxid=122224;
RN [1]
RP SEQUENCE FROM N.A.
RA Wyner Y.M., Johnson S.E., Desalle R.;
RT "A genetic assessment of a red-fronted/white-collared lemur hybrid zone at Andringitra, Madagascar."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF258146; AAK53126.1; -
FT NON_TER 13
SQ SEQUENCE 13 AA; 1327 MM; C105563D492E6D9 CRC64;

Query Match 36.0%; Score 18; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOG 6
DB 4 FVFOG 8

RESULT 21

Q98YC7 PRELIMINARY; PRT; 13 AA.
AC Q98YC7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN POL.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OC NCBI_Taxid=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=992285;
RA Schmidt B., Walter H., Moschik G., Patz C., Wernlein M., Schwingel E., Korn K.;
RT "Recovery of HIV-1 pol gene sequences by direct sequencing of RT amplification products derived from plasma samples."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF347470; AAK32547.1; -
FT NON_TER 13
SQ SEQUENCE 13 AA; 1383 MM; 26583372AF58D878 CRC64;

Query Match 36.0%; Score 18; DB 15; Length 13;
Best Local Similarity 75.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGD 9
DB 6 GGD 9

RESULT 22

Q15902 PRELIMINARY; PRT; 8 AA.
AC Q15902;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE (Clone XP7E7A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32081; AAA73892.1; -
FT NON_TER 8
SQ SEQUENCE 8 AA; 931 MM; 83D699CAB1B2C9 CRC64;

Query Match 34.0%; Score 17; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e-06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
DB 5 DFM 7

RESULT 23

Q90ZV5 PRELIMINARY; PRT; 8 AA.

AC Q90ZV5;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Adenylate kinase (Fragment).
 OS Fulica leucopetra.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Gruiformes; Rallidae; Fulica.
 NCBI_TaxID=156758;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shapiro L.H., Dumbacher J.P.;
 RT "Adenylate kinase intron 5: a new nuclear locus for avian
 RT systematics."
 RL Auk 118:248-255(2001).
 DR EMBL; AF307898; AAK3537.1; -.
 DR GO: GO:0016301; F:kinase activity; IEA.
 KW Kinase.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

Query Match 34.0%; Score 17; DB 13; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 QGGDF 9
 Db 1 QGEEF 5
 RESULT 24
 Q96QAV PRELIMINARY; PRT; 10 AA.
 ID Q96QAV;
 AC Q96QAV;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE BA151A.1 (Cdc42 guanine exchange factor (GEF) 9 (Collypistin, PEM-2,
 DE HPEM-2, KIAA0024)) (Fragment).
 GN ARHGAP9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Whitehead S.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL451106; CAC88408.1; -.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1122 MW; 39925CB878640043 CRC64;

Query Match 34.0%; Score 17; DB 4; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 IGGG 7
 Db 4 IRGG 7
 RESULT 25
 Q47420 PRELIMINARY; PRT; 11 AA.
 ID Q47420;
 AC Q47420;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE ORF1 protein.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92041668; PubMed=1657895;
 RA Sharples G.J., Lloyd R.G.;
 RT "Resolution of Holliday junctions in Escherichia coli: Identification
 RT of the ruvc gene product as a 19-kilodalton protein."
 RL J. Bacteriol. 173:7711-7715(1991).
 DR EMBL; X59551; CAA42127.1; -.
 DR PIR; S19015; S19015.
 SQ SEQUENCE 11 AA; 1215 MW; DB8D5D4D56C6D33D CRC64;

Query Match 34.0%; Score 17; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 QGGD 8
 Db 7 QNGD 10
 RESULT 26
 Q9H1Z6 PRELIMINARY; PRT; 12 AA.
 ID Q9H1Z6;
 AC Q9H1Z6;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Estrogen receptor 1 (Fragment).
 GN ESR1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gonzalez-Gomez F., Vergara F., Pedrosa C., Ramirez J.P.,
 RA Castilla J.A., Yoldi A., Ruiz A., Real L.M.,
 RT "Homo sapiens estrogen receptor 1 (ESR1), intron 1 partial sequence 3'
 RT end".
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF326912; AAG42501.1; -.
 DR GO: GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1385 MW; 09168BCB76C41404 CRC64;

Query Match 34.0%; Score 17; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 QGG 7
 Db 8 QGG 10
 RESULT 27
 O19690 PRELIMINARY; PRT; 13 AA.
 ID O19690;
 AC O19690;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HLA-B protein (Fragment).
 GN HLA-B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood;
 RX MEDLINE=86032060; PubMed=2997032;
 RA Tripan J.A., Mickelson C.A., Deacon N.C., Hooker D.J., McKenzie I.F.;
 RT "Molecular cloning and partial nucleotide sequence of a 3.5 kb HLA-
 RT B27-associated fragment of genomic DNA.";
 RL Immunogenetics 22:399-405(1985).
 DR EMBL: M15634; AAS59615.1; -.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1237 MW; 32C4B4B5B015B5B8 CRC64;

Query Match 34.0%; Score 17; DB 7; Length 13;
 Best Local Similarity 75.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 QGSD 8
 DB 5 QGSD 8

RESULT 28

ID Q883C6 PRELIMINARY; PRT; 9 AA.
 AC Q883C6;
 DT 01-JUN-2002 (TRENBLrel. 21, Created)
 DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE SNF RAD 54-like protein (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot; rosids;
 OC eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Forrest;
 RX MEDLINE=21258784; PubMed=11361330;
 RA Meksem K., Ruden E., Hylen D., Trilwatyakorn K., Lightfoot D.A.;
 RT "Conversion of APLP bands into high-throughput DNA markers.";
 RL Mol. Genet. Genomics 265:207-214(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Forrest;
 RA Meksem K., Lightfoot D., Gibson P.;
 RT "Soybean sudden death syndrome resistant soybeans, soybean cyst
 RT nematode resistant soybeans and methods of breeding and identifying
 RT resistant plants.";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF489439; AAM14563.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1070 MW; DC20A69735A2C699 CRC64;

Query Match 32.0%; Score 16; DB 10; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMI 4
 DB 1 EFMV 4

RESULT 29

ID Q725A2 PRELIMINARY; PRT; 10 AA.
 AC Q725A2;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RA Fratini P., Forss-Petter S., Berger J.;
 RT "A novel relative of Bubbligum.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ575751; CAE12153.1; -.
 FT NON_TER 1
 SQ SEQUENCE 10 AA; 1086 MW; 622094D8786769D4 CRC64;

Query Match 32.0%; Score 16; DB 4; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 FMIQGG 7
 DB 2 FRPPGG 7

RESULT 30

ID O54226 PRELIMINARY; PRT; 12 AA.
 AC O54226;
 DT 01-JUN-1998 (TRENBLrel. 06, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
 DE Polyketide synthase (Fragment).
 OS ERYA.
 OC Saccharopolyspora erythraea (Streptomyces erythraeus).
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Pseudonocardineae; Pseudonocardaceae; Saccharopolyspora.
 OX NCBI_TaxID=1836;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL2338;
 RA Salah-Bey K., Doumith M., Michel J.M., Haydock S., Cortes J.,
 RA Leadlay P.F., Raynal M.C.;
 RT "Targeted gene inactivation for the elucidation of deoxysugar
 RT biosynthesis in the erythromycin producer saccharopolyspora
 RT erythraea.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: Y14332; CAA74712.1; -.
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1282 MW; D4BA3E57E277337D CRC64;

Query Match 32.0%; Score 16; DB 2; Length 12;
 Best Local Similarity 37.5%; Pred. No. 2.2e+04;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPMIOGD 8
 DB 4 DAWLGGSN 11

RESULT 31

ID Q726M4 PRELIMINARY; PRT; 12 AA.
 AC Q726M4;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE D7796117.4 (Novel protein similar to GS2) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Barlow K.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL035396; CAB63074.1; -.
 FT NON_TER 1

SQ SEQUENCE 12 AA; 1430 MW; AF7740ABECB69AA6 CRC64;
Query Match 32.0%; Score 16; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 1 DFMIOG 6
DB 6 DMSFOG 11
RESULT 32
ID 046664 PRELIMINARY; PRT; 12 AA.
AC 046664;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Glucose-6-phosphate dehydrogenase (Fragment).
GN G6PD.
OS Macropus robustus robustus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=35580;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97224585; PubMed=9060417;
RA Loebel D.A., Johnston P.G.;
RT "Analysis of the intron-exon structure of the G6PD gene of the
RT wallaroo (Macropus robustus) by polymerase chain reaction.";
RL Mamm. Genome 8:146-147(1997).
DR EMBL; U53774; AAC48789.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 12 AA; 1430 MW; D42A9C84E3CB1AA9 CRC64;

Query Match 32.0%; Score 16; DB 6; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.2e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

CY 5 QXGDF 9
DB 1 RQGVF 5

RESULT 33

ID 002320 PRELIMINARY; PRT; 12 AA.
AC 002320;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Chalcone synthase (Fragment).
OS Pinus sylvestris (Scots pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3349;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93015948; PubMed=1400374;
RA Schroder G., Schroder U.;
RT "A single change of histidine to glutamine alters the substrate
RT preference of a stilbene synthase.";
RL J. Biol. Chem. 267:20558-20560(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=92163014; PubMed=1336925;
RA Flegmann U., Schroder G., Schanz S., Britsch L., Schroder U.;
RT "Molecular analysis of chalcone and dihydroquercetin synthase from
RT Scots pine (Pinus sylvestris), and differential regulation of these
RT and related enzyme activities in stressed plants.";
RL Plant Mol. Biol. 18:489-503(1992).
RN [3]

RP SEQUENCE FROM N.A.
RA Schroder U.;
RL Submitted (Aug-1992) to the EMBL/GenBank/DBJ databases.
DR EMBL; L00658; AAA50523.1; -.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1303 MW; EDB35A1BE0CEB871 CRC64;
Query Match 32.0%; Score 16; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.2e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 3 MIOGDF 9
DB 2 MYOQGF 8

RESULT 34

ID 038715 PRELIMINARY; PRT; 12 AA.
AC 038715;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Resveratrol synthase (Fragment).
OS Arachis hypogaea (Peanut).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eustosids I; Fabales; Fabaceae; Papilionoideae; Aeschynomeneae;
OC Arachis.
OX NCBI_TaxID=3818;
RN [1]
RP SEQUENCE FROM N.A.
RA Lanz T., Schroder G., Schroder U.;
RT "Differential regulation of genes for resveratrol synthase in cell
RT cultures of Arachis hypogaea L.";
RL Planta 181:169-175(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=9126783; PubMed=2033084;
RA Schroder U.;
RT "The role of cysteines in polyketide synthases. Site-directed
RT mutagenesis of resveratrol and chalcone synthases, two key enzymes in
RT different plant specific pathways.";
RL J. Biol. Chem. 266:9971-9976(1991).
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE=93015948; PubMed=1400374;
RA Schroder G., Schroder U.;
RT "A single change of histidine to glutamine alters the substrate
RT preference of a stilbene synthase.";
RL J. Biol. Chem. 267:20558-20560(1992).
DR EMBL; L00953; AAC41685.1; -.
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1294 MW; COB35A1BE0CEB866 CRC64;

Query Match 32.0%; Score 16; DB 10; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.2e+04;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 3 MIOGDF 9
DB 2 MYOQGF 8

RESULT 35

ID 093824 PRELIMINARY; PRT; 13 AA.
AC 093824;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE UDP-galactose-4-epimerase (Fragment).
GN GAL10.

OS Candida tropicalis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OC NCB1_TaxID=5482;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PK233;
 RA Kanai T., Ueda M., Tanaka A.;
 RT "Candida tropicalis promoter region of GAL1 and GAL10 gene.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB019434; BAA34351.1; -
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1312 MW; 0B559D6AE18BC720 CRC64;
 Query Match 32.0%; Score 16; DB 3; Length 13;
 Best Local Similarity 40.0%; Pred. NO. 2.3e+04;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Oy 3 MIOGG 7
 Db 7 LVTGG 11
 RESULT 36
 Q39380 PRELIMINARY; PRT; 13 AA.
 AC Q39380;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE IFA binding protein (Sp10) (Fragment).
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eustids; IT; Brassicales; Brassicaceae; Brassica.
 OC NCB1_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DK; TISSUE=Curd surface;
 RA Willis G.;
 RT "An investigation of nuclear lamin homologues in plants: an apparently non-intermediate filament sequence that bind a polyclonal anti-lamin antiserum."
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X97678; CAA66268.1; -
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1413 MW; D1D4EA3926B42772 CRC64;
 Query Match 32.0%; Score 16; DB 10; Length 13;
 Best Local Similarity 50.0%; Pred. NO. 2.3e+04;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Oy 5 QGGD 8
 Db 9 EGGE 12
 RESULT 37
 Q814P5 PRELIMINARY; PRT; 14 AA.
 AC Q814P5;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Beta-expansin-like protein (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OC NCB1_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Various strains;
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
 RA Morgante M., Rafalski J.A.;
 RT "SNP frequency, haplotype structure and linkage disequilibrium in elite maize inbred lines."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY094284; AAM21810.1; -
 DR EMBL; AY094285; AAM21811.1; -
 DR EMBL; AY094286; AAM21812.1; -
 DR EMBL; AY094287; AAM21813.1; -
 DR EMBL; AY094288; AAM21814.1; -
 DR EMBL; AY094289; AAM21815.1; -
 DR EMBL; AY094290; AAM21816.1; -
 DR EMBL; AY094291; AAM21817.1; -
 DR EMBL; AY094292; AAM21818.1; -
 DR EMBL; AY094293; AAM21819.1; -
 DR EMBL; AY094294; AAM21820.1; -
 DR EMBL; AY094295; AAM21821.1; -
 DR EMBL; AY094296; AAM21822.1; -
 DR EMBL; AY094297; AAM21823.1; -
 DR EMBL; AY094298; AAM21824.1; -
 DR EMBL; AY094299; AAM21825.1; -
 DR EMBL; AY094300; AAM21826.1; -
 DR EMBL; AY094301; AAM21827.1; -
 DR EMBL; AY094302; AAM21828.1; -
 DR EMBL; AY094303; AAM21829.1; -
 DR EMBL; AY094304; AAM21830.1; -
 DR EMBL; AY094305; AAM21831.1; -
 DR EMBL; AY094306; AAM21832.1; -
 DR EMBL; AY094307; AAM21833.1; -
 DR EMBL; AY094311; AAM21837.1; -
 DR EMBL; AY094312; AAM21838.1; -
 DR EMBL; AY094313; AAM21839.1; -
 DR EMBL; AY094314; AAM21840.1; -
 DR EMBL; AY094315; AAM21841.1; -
 DR EMBL; AY094316; AAM21842.1; -
 DR EMBL; AY094317; AAM21843.1; -
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1537 MW; 5C5SEBD1391BBA3 CRC64;
 Query Match 32.0%; Score 16; DB 10; Length 14;
 Best Local Similarity 37.5%; Pred. NO. 2.5e+04;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 DFMIQGD 8
 Db 1 EFVIAKSD 8
 RESULT 38
 Q86578 PRELIMINARY; PRT; 14 AA.
 AC Q86578;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Protein 4 (Fragment).
 GN 4.
 OS Sigma virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; unclassified Rhabdoviridae.
 OC NCB1_TaxID=11301;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINB=93212481; PubMed=8384742;
 RA Teninges D., Bras F., Dezelee S.;
 RT "Genome organization of the sigma rhabdovirus: six genes and a gene overlap."
 RL Virology 193:1018-1023 (1993).
 DR EMBL; S57855; AAD40703.1; -
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1549 MW; 397C3BDAD3E4CA08 CRC64;

Query Match 32.0%; Score 16; DB 12; Length 14;
 Best Local Similarity 25.0%; Pred. No. 2.5e+04;
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 FMIOGDP 9
 : : : :
 : : : :
 Db 2 YSLTGGY 9

RESULT 39

Q88400 PRELIMINARY; PRT; 14 AA.
 AC Q88400;
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Tax protein (Fragment).
 GN TAX.
 OS Simian T-lymphotropic virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Deltaretrovirus.
 CX NCBI_TaxID=33747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94082462; PubMed=8259665;
 RA Saksena N.K., Harve V., Durand U.P., LeGuerno B., Diop O.M.,
 RA DiGoutte J.P., Mathiot C., Muller M.C., Love J.L., Benz P.M.,
 RA Bensenoy S., Barre-Sinoussi F., Poles B.J.,
 RT "Seroepidemiologic, molecular, and phylogenetic analyses of simian T-
 cell leukemia viruses (STLV-I) from various naturally infected monkey
 RT species from central and western Africa.";
 RL Virology 198;297-310(1993).
 DR EMBL; L20363; AAA47870.1; -
 DR GO; GO:0016563; F:transcriptional activator activity; IRA.
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.
 DR InterPro; IPR004120; Tax.
 DR Pfam; PF02959; Tax; 1.
 FT NON_TER 1
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1394 MW; 8BA7726C9C6D387A CRC64;

Query Match 32.0%; Score 16; DB 15; Length 14;
 Best Local Similarity 75.0%; Pred. No. 2.5e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IOGG 7
 : : : :
 : : : :
 Db 11 ISGG 14

RESULT 40

Q8UT17 PRELIMINARY; PRT; 14 AA.
 ID Q8UT17;
 AC Q8UT17;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Gag protein.
 GN Gag.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 CX NCBI_TaxID=11676;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=08M2127.214;
 RC Novitsky V.A., Smith U.R., Gilbert P., McLane M.F., Chigwedere P.,
 RA Williams C., Ngunjiri T., Klein I., Chang S.-Y., Peter T., Thior I.,
 RA Foley B.T., Golekwe S., Rybak N., Gasetlwe S., Vanberg F.,
 RA Marink R., Lee T.-H., Essex M.,
 RT "HIV-1 subtype C molecular phylogeny: consensus sequence for an AIDS
 RT vaccine design.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF443105; AAL34832.1; -
 SQ SEQUENCE 14 AA; 1486 MW; 1F8F11F22AA03E20 CRC64;

Query Match 32.0%; Score 16; DB 15; Length 14;
 Best Local Similarity 40.0%; Pred. No. 2.5e+04;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOGG 7
 : : : :
 : : : :
 Db 7 ILRGG 11

RESULT 41

Q9POK3 PRELIMINARY; PRT; 8 AA.
 ID Q9POK3;
 AC Q9POK3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE GMP-specific phosphodiesterase PDE5A2 (Fragment).
 GN PDE5A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20145478; PubMed=10679249;
 RA Lin C.S., Lau A., Tu R., Lue T.F.,
 RT "Identification of three alternative first exons and an intronic
 RT promoter of human PDE5A gene.";
 RL Biochem. Biophys. Res. Commun. 268:596-602(2000).
 DR EMBL; AF151951; AAF40302.1; -
 DR GO; GO:0004116; F:GMP-specific phosphodiesterase activity; NAS.
 FT NON_TER 8
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 908 MW; E8A33AA879D76726 CRC64;

Query Match 30.0%; Score 15; DB 4; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 MIOGCD 8
 : : : :
 : : : :
 Db 1 MLPFGD 6

RESULT 42

Q9BOT4 PRELIMINARY; PRT; 9 AA.
 ID Q9BOT4;
 AC Q9BOT4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE CLIP-associating protein CLASP2 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RC Galjart N.,
 RA Galjart N.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RX MEDLINE=21185938; PubMed=11290329;
 RA Akhmanova A., Hoogenraad C.C., Dyrek K., Stepanova T., Dordland B.,
 RA Verkerk T., Vermeulen W., Burgering B.M., de Zeeuw C.I., Grosveld F.,
 RA Galjart N.,
 RT "CLASPs are CLIP-115 and -170 associating proteins involved in the
 RT regional regulation of microtubule dynamics in motile fibroblasts.";
 RL Cell 104:923-935(2001)
 DR EMBL; A0288058; CAC35157.1; -
 DR GO; GO:0005737; C:cytoplasm; NAS.

DR GO: GO:0008107; F:galactoside 2-alpha-L-fucosyltransferase ac. . .; NAS.
 DR GO: GO:0007026; P:microtubule stabilization; NAS.

FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1001 MW; C3ECB33AAA8769D CRC64;

Query Match 30.0%; Score 15; DB 4; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 MIOGCD 8
 DB 1 MAMGDD 6

RESULT 43

ID Q92009 PRELIMINARY; PRT; 9 AA.

AC Q92009; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE C-REL protein (Fragment).

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;

OC Gallus.

OX NCB1_TaxID=9031;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91133736; PubMed=2284104;

RA Hannink M., Temin H.M.;

RT "Structure and autoregulation of the c-rel promoter.";

RL Oncogene 5:1843-1850(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX Oncogene 0:0-0(1990).

RA Hannink M., Temin H.M.;

RL Oncogene 0:0-0(1990).

DR EMBL; X56440; CAA39822.1; -;

DR EMBL; X56515; CAA39866.1; -;

PIR; I50633; I50633.

FT NON_TER 9

SQ SEQUENCE 9 AA; 805 MW; DE317DD87865A2CD CRC64;

Query Match 30.0%; Score 15; DB 13; Length 9;

Best Local Similarity 50.0%; Pred. No. 1e+06; 1; Indels 0; Gaps 0;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 IOGG 7

DB 3 VSGG 6

RESULT 44

ID Q9HFN8 PRELIMINARY; PRT; 11 AA.

AC Q9HFN8; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

DE Acyl carrier protein (Fragment).

GN ACP.

OS Candida rugosa (Yeast) (Candida cylindracea).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCB1_TaxID=5481;

RN [1]

RP SEQUENCE FROM N.A.

RA Blasio W.;

RL Thesis (2000), University of Vienna, Austria.

DR EMBL; AJ279021; CAC08812.1; -;

FT NON_TER 1

SQ SEQUENCE 11 AA; 1274 MW; D2B4CG376C40732 CRC64;

Query Match 30.0%; Score 15; DB 3; Length 11;
 Best Local Similarity 25.0%; Pred. No. 3e+04; 2; Indels 0; Gaps 0;
 Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPMIOGCD 8
 DB 2 DYVLQPD 9

RESULT 45

ID 077876 PRELIMINARY; PRT; 11 AA.

AC 077876; 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE MAC class II B locus 1 (Fragment).

OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroides;

OC Cichlidae; Oreochromis.

OX NCB1_TaxID=8128;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98315113; PubMed=9649539;

RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vencek V.,

RA Figueroa F., Sultmann H., Klein J.;

RT "Linkage relationships and haplotype polymorphism among cichlid mhc

RL class II B loci.";

DR Genetics 149:1527-1537(1998).

DR EMBL; AF049985; AAC41324.1; -;

FT NON_TER 1

SQ SEQUENCE 11 AA; 1178 MW; 9AC131FAB2D2DB45 CRC64;

Query Match 30.0%; Score 15; DB 7; Length 11;

Best Local Similarity 28.6%; Pred. No. 3e+04; 2; Indels 0; Gaps 0;

Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGCD 8

DB 5 YVVTGCD 11

Search completed: August 30, 2004, 10:55:13

Job time : 12.6655 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 ; Search time 1.55068 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469a-2

Perfect score: 50

Sequence: 1 DFM1QGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Score No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	42.0	14	1	PI4452 equus caball
2	20	40.0	12	1	PI7645 drosophila
3	18	36.0	8	1	PI9990 leucophaea
4	18	36.0	8	1	P23396 locusta mig
5	18	36.0	9	1	P01158 oryctolagus
6	17.5	35.0	10	1	P81012 schizaphis
7	17	34.0	8	1	PI4863 calliphora
8	17	34.0	9	1	PI4856 calliphora
9	17	34.0	9	1	PI4857 calliphora
10	17	34.0	9	1	PI4858 calliphora
11	17	34.0	9	1	PI4859 calliphora
12	17	34.0	9	1	PI4860 calliphora
13	17	34.0	9	1	PI4861 calliphora
14	17	34.0	9	1	PI4862 calliphora
15	17	34.0	9	1	PI4863 calliphora
16	17	34.0	9	1	PI4864 calliphora
17	17	34.0	9	1	PI4865 calliphora
18	17	34.0	9	1	PI4866 calliphora
19	17	34.0	9	1	PI4867 calliphora
20	17	34.0	9	1	PI4868 calliphora
21	17	34.0	9	1	PI4869 calliphora
22	16	32.0	9	1	PI4870 calliphora
23	16	32.0	9	1	PI4871 calliphora
24	16	32.0	9	1	PI4872 calliphora
25	16	32.0	9	1	PI4873 calliphora
26	16	32.0	9	1	PI4874 calliphora
27	16	32.0	9	1	PI4875 calliphora
28	16	32.0	9	1	PI4876 calliphora
29	15	30.0	10	1	PI4877 calliphora
30	15	30.0	10	1	PI4878 calliphora
31	15	30.0	10	1	PI4879 calliphora
32	15	30.0	10	1	PI4880 calliphora
33	15	30.0	10	1	PI4881 calliphora

34	14	28.0	8	1	PI4882 calliphora
35	14	28.0	8	1	PI4883 calliphora
36	14	28.0	8	1	PI4884 calliphora
37	14	28.0	10	1	PI4885 calliphora
38	14	28.0	10	1	PI4886 calliphora
39	14	28.0	10	1	PI4887 calliphora
40	14	28.0	11	1	PI4888 calliphora
41	14	28.0	13	1	PI4889 calliphora
42	14	28.0	13	1	PI4890 calliphora
43	14	28.0	13	1	PI4891 calliphora
44	14	28.0	13	1	PI4892 calliphora
45	14	28.0	14	1	PI4893 calliphora

ALIGNMENTS

RESULT 1	PI4882 calliphora	STANDARD;	PRT;	14 AA.
AC	PI4882			
DT	01-JAN-1990 (Rel. 13, Created)			
DT	01-JAN-1990 (Rel. 13, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Fibrinogen alpha chain [contains: Fibrinopeptide A] (Fragment).			
GN	FCG.			
OS	Equus caballus (Horse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Perissodactyla; Equidae; Equus.			
OX	NCBI_TaxID=9796;			
RM	[1]			
RP	SEQUENCE.			
RA	Blomback M., Blomback M., Grondahl N.J.;			
RT	"Studies on fibrinopeptides from mammals."			
RL	Acta Chem. Scand. 19:1789-1791(1965).			
CC	-1- FUNCTION: Fibrinogen has a double function: yielding monomers that polymerize into fibrin and acting as a cofactor in platelet aggregation.			
CC	-1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.			
CC	-1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves fibrinopeptides A and B from alpha and beta chains, and thus exposes the N-terminal polymerization sites responsible for the formation of the soft clot.			
KW	Blood coagulation; Plasma.			
FT	PEPTIDE 1 14 FIBRINOPEPTIDE A.			
FT	NON TER 14			
SQ	SEQUENCE 14 AA; 1517 MW; 4E998EB63C2A15E7 CRC64;			
QY	Query Match	42.0%;	Score 21;	DB 1; Length 14;
Db	Best local Similarity	42.9%;	Pred. No. 3,4e+02;	
	Matches 3; Conservative	3;	Mismatches 1;	Indels 0; Gaps 0;
	5 EFM1QGG 7			
	5 EFM1QGG 11			
RESULT 2	OP33 DROVI	STANDARD;	PRT;	12 AA.
AC	PI7645			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	01-AUG-1990 (Rel. 15, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Opsin Rh3 (inner R7 photoreceptor cells opsin) (Fragment).			
GN	Rh3.			
OS	Drosophila virilis (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7244;			
RM	[1]			

RP SEQUENCE FROM N.A.
 RX MEDLINE=90249748; PubMed=2140105;
 RA Fortini M.E., Rubin G.M.;
 RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals
 a bipartite organization to rhodopsin promoters in *Drosophila*
 melanogaster";
 RL Genes Dev. 4:444-463(1990).
 CC -1- FUNCTION: Visual pigments are the light-absorbing molecules that
 mediate vision. They consist of an apoprotein, opsin, covalently
 linked to cis-retinal.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- MISCELLANEOUS: Each *Drosophila* eye is composed of 800 facets or
 ommatidia. Each ommatidium contains 8 photoreceptor cells (R1-R8),
 the R1 to R6 cells are outer cells, while R7 and R8 are inner
 cells.
 CC -1- MISCELLANEOUS: Opsin Rh3 is sensitive to UV light.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC Opsin subfamily.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; X51350; CAA5742.1; -
 DR FlyBase; FBgn0013091; Dv1tRh3.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR001760; Opsin.
 DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; PARTIAL.
 DR PROSITE; PS00238; OPSIN; PARTIAL.
 KW Photoreceptor; Retinal protein; Transmembrane; Phosphorylation;
 KM Glycoprotein; G-protein coupled receptor; Vision.
 FT CARBOHYD 10 10 N-LINKED (GLCNAC . .) (PROBABLE).
 FT NON TER 12 12
 FT SEQUENCE 12 AA; 1253 MW; 04024E43495865B0 CRC64;
 SQ
 Query Match 40.0%; Score 20; DB 1; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFMIG 6
 DB 2 DFMIG 7

RESULT 3
 LCK8 LEUMA STANDARD; PRT; 8 AA.
 AC P19930;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Leucokinin VIII (L-VIII).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 CC Blaberidae; Leucophaea.
 CC NCBI_TaxID=6988;
 CC (1)
 RN SEQUENCE.
 RP TISSUE=Head;
 RC Holman G.M., Cook B.J., Nachman R.J.;
 RT "Isolation, primary structure and synthesis of leucokinin VII and
 VIII: the final members of this new family of cephalomyotropic
 peptides isolated from extracts of *Leucophaea maderae*.";
 RL Comp. Biochem. Physiol. 88C:31-34(1987).
 CC -1- FUNCTION: This cephalomyotropic peptide stimulates contractile
 activity of cockroach procoelom (hindgut).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 DR PIR; JS0318; JS0318.

KM Neuropeptide; Amidation.
 FT MOD RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA; 902 MW; 736365AB59CAADB8 CRC64;
 Query Match 36.0%; Score 18; DB 1; Length 8;
 Best Local Similarity 75.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GDF 9
 DB 1 GDF 4

RESULT 4
 LMT2 LOCMI STANDARD; PRT; 8 AA.
 ID LMT2 LOCMI
 AC P22336;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DE Locustamyotropin 2 (LOM-MT-2).
 CC Locusta migratoria (Migratory locust).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
 CC Acridoidea; Acrididae; Caelipodinae; Locusta.
 CC NCBI_TaxID=7004;
 CC (1)
 RN SEQUENCE.
 RP TISSUE=Corpora cardiaca;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin II, an
 additional neuropeptide of *Locusta migratoria*. Member of the
 cephalomyotropic peptide family.";
 RL Insect Biochem. 20:479-484(1990).
 CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
 activity).
 CC -1- SIMILARITY: Belongs to the pyrokinin family.
 CC InterPro: IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ_1.
 KM Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8 8 AMIDATION.
 FT SEQUENCE 8 AA; 934 MW; 26341771A9CAAB7B CRC64;
 SQ
 Query Match 36.0%; Score 18; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GDF 9
 DB 2 GDF 4

RESULT 5
 DSIP RABIT STANDARD; PRT; 9 AA.
 ID DSIP RABIT
 AC P01158;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Delta sleep-inducing peptide (DSIP).
 OS *Oryzolagus cuniculus* (Rabbit).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryzologiagus.
 CC NCBI_TaxID=9986;
 CC (1)
 RN SEQUENCE.
 RP MEDLINE=77185324; PubMed=862769;
 RX Wondner M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
 RA Schenkenberger G.A.;
 RT "The delta sleep inducing peptide (DSIP). Comparative properties of
 the original and synthetic nonapeptide.";
 RL Experientia 33:548-552(1977).
 RL [2]

RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=79054421; PubMed=568769;
 RA Schoenberg G.A., Mater P.F., Tobler H.J., Wilson K., Monnier M.;
 RT "The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
 RT analysis, sequence, synthesis and activity of the nonapeptide.";
 RL Pflugers Arch. 366:119-129(1978).
 RN [3]
 RP REVIEW.
 RX MEDLINE=87175129; PubMed=3550726;
 RA Graf M.V., Kastin A.J.;
 RT "Delta-sleep-inducing peptide (DSIP): an update.";
 RL Peptides 7:1165-1187(1986).
 CC -1- FUNCTION: When infused into the mesodiencephalic ventricle of
 CC recipient rabbits induces spindle and delta EEG activity and
 CC reduced motor activities.
 CC -1- MISCELLANEOUS: This peptide was obtained from dialysates of
 CC occipital venous sinus blood from rabbits kept asleep by electric
 CC stimulation of the thalamus.
 CC -1- DATABASE: NAME=Protein SpotLight;
 CC NOTE=Issue 8 of March 2003;
 CC WWW="http://www.easys.org/spotlight/articles/spc1008.html".
 DR PIR: A01422; QDRB.
 SQ SEQUENCE 9 AA; 849 MW; DDD365BDAA8787D CRC64;

Query Match 36.0%; Score 18; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Mismatches 0; Gaps 0;
 Matches 3; Conservative 0; Indels 0;

OY 6 GGD 8
 Db 3 GGD 5

RESULT 6
 ESTA_SCHGA STANDARD; PRT; 10 AA.
 ID _ESTA_SCHGA
 AC P81012;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last annotation update)
 DE Esterase 52 kDa subunit (EC 3.1.1.1) (Carboxylic-ester hydrolase)
 OS (Fragmant).
 OS Schizaphis graminum (Aphid).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha; Aphidiformes;
 OC Aphidoidea; Aphididae; Aphidini; Schizaphis.
 CC NCBI_TaxID=13262;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97468499; PubMed=9327586;
 RA Siegfried B.D., Ono M., Swanson J.J.;
 RT "Purification and characterization of a carboxylesterase associated
 RT with organophosphate resistance in the greenbug, Schizaphis graminum
 RT (Homoptera: Aphididae).";
 RL Arch. Insect Biochem. Physiol. 36:229-240(1997).
 CC -1- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
 CC carboxylic anion.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
 DR InterPro: IPR002018; Carboxylesterase.
 DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; PARTIAL.
 DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; PARTIAL.
 KM Hydrolyse: Serine esterase.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1025 MW; 018ABE587865A2C0 CRC64;

Query Match 35.0%; Score 17.5; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.2e+03; Mismatches 1; Gaps 1;
 Matches 4; Conservative 2; Indels 1;

OY 3 MIQG-DF 9
 Db 3 IVSGGYDF 10

RESULT 7
 FARP_CALVO STANDARD; PRT; 8 AA.
 ID _FARP_CALVO
 AC P41863;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRamide 8.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 CC NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Dive H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rahfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Net-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 DR PIR: H41978; H41978.
 KM Neuropeptide; Amidation.
 FT MOD_RES 8 8
 SQ SEQUENCE 8 AA; 957 MW; 72D40699CAA44D8 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05; Mismatches 0; Gaps 0;
 Matches 3; Conservative 0; Indels 0;

OY 1 DFM 3
 Db 4 DFM 6

RESULT 8
 FARP_CALVO STANDARD; PRT; 9 AA.
 ID _FARP_CALVO
 AC P41856;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CalliFMRamide 1.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 CC NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Dive H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rahfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Net-Arg-Phe-NH2
 RT neuropeptides (designated calliFMRamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- FUNCTION: Able to induce fluid secretion from the isolated
 CC salivary gland of Calliphora.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 CC family.
 DR PIR: A41978; A41978.
 KM Neuropeptide; Amidation.
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 1169 MW; 29D00699CAB66C7 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
5 DFM 7

RESULT 9

FAR2 CALVO STANDARD; PRT; 9 AA.

AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- FUNCTION: Able to induce fluid secretion from the isolated
salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; B41978; B41978.
KM Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1128 MW; 29D00699CAB5C5A7 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
5 DFM 7

RESULT 10

FAR3 CALVO STANDARD; PRT; 9 AA.

AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

CC -1- FUNCTION: Able to induce fluid secretion from the isolated
salivary gland of Calliphora.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; C41978; C41978.
KM Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB5C5A7 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
5 DFM 7

RESULT 11

FAR4 CALVO STANDARD; PRT; 9 AA.

AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 4.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRamides) from the blowfly
Calliphora vomitoria.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; D41978; D41978.
KM Neuropeptide; Amidation.
FT MOD_RES 9
SQ SEQUENCE 9 AA; 1182 MW; 31730699CAB5D457 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
5 DFM 7

RESULT 12

FAR5 CALVO STANDARD; PRT; 9 AA.

AC P41860;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 5.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;

RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifmrfamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -I- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR: E41978; E41978.
 KM Neuropeptide; Amidation.
 FT MOD RES
 SQ SEQUENCE 9 AA; 1068 MW; 39D1069CAB6D867 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
 |||
 Db 5 DFM 7

RESULT 13
 FAP6_CALVO STANDARD; PRT; 9 AA.
 ID FAP6_CALVO
 AC P41861;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callifmrfamide 6.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 CC NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifmrfamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -I- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR: F41978; F41978.
 KM Neuropeptide; Amidation.
 FT MOD RES
 SQ SEQUENCE 9 AA; 1058 MW; 96D1069CAB6D865 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
 |||
 Db 5 DFM 7

RESULT 14
 FAP7_CALVO STANDARD; PRT; 9 AA.
 ID FAP7_CALVO
 AC P41862;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callifmrfamide 7.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OC Calliphoridae; Calliphora.
 CX NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifmrfamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -I- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR: G41978; G41978.
 KM Neuropeptide; Amidation.
 FT MOD RES
 SQ SEQUENCE 9 AA; 1081 MW; E1D1069CAB6D86A CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
 |||
 Db 5 DFM 7

RESULT 15
 FAP8_CALVO STANDARD; PRT; 9 AA.
 ID FAP8_CALVO
 AC P41863;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callifmrfamide 10.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 CC NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Thoracic ganglion;
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duvé H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
 Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifmrfamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -I- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 CC family.
 DR PIR: A44787; A44787.
 KM Neuropeptide; Amidation.
 FT MOD RES
 SQ SEQUENCE 9 AA; 1183 MW; 29D0069CAB40457 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
 |||
 Db 5 DFM 7

RESULT 16
 FAP9_CALVO STANDARD; PRT; 9 AA.
 ID FAP9_CALVO
 AC P41864;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callifmrfamide 11.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;

DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neb-FMRamide 1.
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Sarcophagidae; Sarcophaga.
 NCBI_TaxID=7385;
 RN [1]
 RP SEQUENCE, AMIDATION, AND FUNCTION.
 RC TISSUE=CNS;
 RX MEDLINE=22342733; PubMed=12438685;
 RA Meusen T., Mertens I., Clynen E., Baggerman G., Nichols R.,
 RA Nachman R.J., Huybrechts R., De Loof A., Schoofs L.;
 RT "Identification in *Drosophila melanogaster* of the invertebrate G
 protein-coupled FMRamide receptor".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:15363-15368(2002).
 CC -1- FUNCTION: Has modulatory actions at skeletal neuromuscular
 junctions.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the FMR (FMRamide related peptide)
 family.
 KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1155 MW; 2D810699CAB6C5A7 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
 Db 5 DFM 7

RESULT 17
 ID THYF_PIG STANDARD; PRT; 9 AA.
 AC P01255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78026571; PubMed=914862;
 RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-P.;
 RT "Structural study of circulating thymic factor: a peptide isolated
 from pig serum. II. Amino acid sequence.";
 RL J. Biol. Chem. 252:8045-8047(1977).
 CC -1- MISCELLANEOUS: The biological source(s) and physiological
 activities of this peptide have not been determined.
 DR PIR: A01523; YFPG.
 KM Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 1 1
 FT MOD_RES 9 9
 SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B3D CRC64;

Query Match 34.0%; Score 17; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
 Db 5 QGG 7

RESULT 18
 BPP4_BOTIN

ID BPP4_BOTIN STANDARD; PRT; 11 AA.
 AC P30424;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,1,2 (Angiotensin-converting
 DE enzyme inhibitor).
 OS Bothrops insularis (Island jararaca) (Queimada jararaca).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Viperidae; Crotalinae; Bothrops.
 NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintrá A.C.O., Vieira C.A., Gaglió J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 RT peptides from *Bothrops insularis* snake venom".
 RL J. Protein Chem. 9:221-227(1990).
 CC -1- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR: D37196; D37196.
 KM Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1143 MW; 20BBB313C7741777 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
 Db 1 QGG 3

RESULT 19
 ID FAR9_CALVO STANDARD; PRT; 11 AA.
 AC P41864;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Callifmrfamide 9.
 OS Calliphora vomitoria (Blue blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Calliphoridae; Calliphora.
 NCBI_TaxID=27454;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92196111; PubMed=1549595;
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated callifmrfamides) from the blowfly
 RT Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: Belongs to the FMR (FMRamide related peptide)
 family.
 DR PIR: I41978; I41978.
 KM Neuropeptide; Amidation.
 FT MOD_RES 11 11
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA; 1359 MW; 8160CE46CNA44321 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3

Db 7 DFM 9

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RESULT 20
BOWL_PSEGU STANDARD; PRT; 13 AA.
AC P42931;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Bombesin-like peptide I (Pg-L).
OS Pseudophryne guentheri (Guenther's toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Myobatrachinae; Pseudophryne.
OX NCBI_TaxID=30349;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=90287814; PubMed=2356157;
RA Simeaco M., Severini C., de Biase D., Barra D., Bossa F.,
RA Roberts J.D., Melchiorri P., Brspamer V.;
RT "Six novel tachykinin- and bombesin-related peptides from the skin of
RL the Australian frog Pseudophryne guentheri.";
RL Peptides 11:299-304(1990).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the bombesin/neurotensin B/ratanensin
CC family.
DR PIR; A60409; A60409.
DR InterPro; IPR000874; Bombesin.
DR Pfam; PF02044; Bombesin. 1.
DR PROSITE; PS00257; BOMBESIN; 1.
KW Amphibian defense peptide; Bombesin family; Amidation;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 13 AMIDATION.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1372 MW; D6DED024BD98C366 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
Db 1 QGG 3

RESULT 21
BPI BOTJA STANDARD; PRT; 13 AA.
ID BPI BOTJA STANDARD; PRT; 13 AA.
AC P01020; P30421;
DT 21-JUL-1996 (Rel. 01, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S3,1 (13a) (Angiotensin-converting
DE enzyme inhibitor V-9).
OS Bothrops jararaca (Jararaca), and
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroslossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724; 8723;
RN [1]
RP SEQUENCE.
RC SPECIES=B. jararaca; TISSUE=Venom;
RX MEDLINE=72118526; PubMed=4334402;
RA Ondetti M.A., Williams N.J., Sado E.F., Pluscec J., Weaver E.R.,
RA Kocay O.;
RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
RT jararaca. Isolation, elucidation of structure, and synthesis.";
RT Biochemistry 10:4033-4039(1971).

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RN [2]
RP SEQUENCE.
RC SPECIES=B. insularis; TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; A01253; XAVI9B.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 13 AMIDATION.
FT MOD_RES 13 13 AMIDATION.
SQ SEQUENCE 13 AA; 1388 MW; 6824FC97D83D6774 CRC64;

Query Match 34.0%; Score 17; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
Db 1 QGG 3

RESULT 22
ALLS CYDPO STANDARD; PRT; 8 AA.
ID ALLS CYDPO STANDARD; PRT; 8 AA.
AC P82156;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiaetatin 5.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=8054539; PubMed=9392829;
RA Davey M., Johnson A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).
CC -1- SIMILARITY: Belongs to the allatostatin family.
KW Neuropeptide; Amidation.
FT MOD_RES 8 8 AMIDATION.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 898 MW; 922879CAB85640D CRC64;

Query Match 32.0%; Score 16; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QGGDF 9
Db 2 RGYDF 6

RESULT 23
DL NEPNO STANDARD; PRT; 9 AA.
ID DL NEPNO STANDARD; PRT; 9 AA.
AC P24816;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Gastrin/cholecystokinin-like peptide D1.
OS Nephrops norvegicus (Norway lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Ascaridea;
OC Nephropoidea; Nephropidae; Nephrops.

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OX NCBI_TaxID=6829;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RA MEDLINE=92082847; PubMed=1747388; Kellier R., van Wormhoudt A.;
RX Favre P., Kegel G., Sedimeier D.,
RT "Structure and biological activity of crustacean gastrointestinal
RL peptide identified with antibodies to gastrin/cholecystokinin.";
RM Biochimie 73:1233-1239(1991).
CC -1- FUNCTION: May control digestion processes in crustaceans.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR PIR; S47432; S47432.
KW Hormone.
SQ SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 1; Length 9;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GPDF 9
DB 4 GPDF 7

RESULT 24
ID FIBA_CAVPO STANDARD; PRT; 13 AA.
AC P14445;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE.
RA Blomback B., Blomback M., Grondahl N.J.;
RT "Studies on fibrinopeptides from mammals.";
RL Acta Chem. Scand. 19:1789-1791(1965).
CC -1- FUNCTION: Fibrinogen has a double function: Yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 13 FIBRINOPEPTIDE A.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1309 MW; 639999286C79DDDB CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 1; Length 13;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
DB 4 EFPAAGG 10

RESULT 25
ID PROX_ORYSA STANDARD; PRT; 13 AA.
AC P83647;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable profilin LP04 (Fragments).

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OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoideae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA STRAIN=cv. Indica-IR64; TISSUE=Panicle;
RX Hosseini Salekdeh S.G., Bennett J.;
RT "Proteome analysis of rice panicle.";
RM Submitted (GUL-2003) to Swiss-Prot.
CC -1- FUNCTION: Binds to actin and affects the structure of the
CC cytoskeleton. At high concentrations, profilin prevents the
CC polymerization of actin, whereas it enhances it at low
CC concentrations. By binding to p1p2, it inhibits the formation of
CC IP3 and DG (By similarity).
CC -1- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric
CC actin in a 1:1 ratio.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.4, its MW is: 14.0 kDa.
CC -1- SIMILARITY: Belongs to the profilin family.
DR PROSITE; PS00414; PROFILIN; PARTIAL.
KW Actin-binding; Cytoskeleton; Multigene family.
FT NON_TER 1 1
FT NON_CONS 5 6
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1362 MW; 0A3022EB0E52C68B CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 1; Length 13;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOG 6
DB 8 VIOG 11

RESULT 26
ID SA2A_ONCMY STANDARD; PRT; 13 AA.
AC P82238;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Salmocidin 2A (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Serum;
RA Henry M.A., Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides
RT from rainbow trout, Oncorhynchus mykiss.";
RL Submitted (DEC-1999) to Swiss-Prot.
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1416 MW; 5FFB792AFC645873 CRC64;

Query Match
Best Local Similarity 32.0%; Score 16; DB 1; Length 13;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FMIOG 6
DB 3 FVLKG 7

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RESULT 27
SA2B_ONCMY STANDARD; PRT; 13 AA.
ID P82239;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Salmocidin 2B (Fragment).
OS Oncochrychus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proacanthopterygii; Salmoniformes; Salmonidae; Oncochrychus.
OX NCBI_TaxID=8022;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Serum;
RA Henry M.A., Secombes C.J.;
RT "Purification and partial characterization of antibacterial peptides
RT from rainbow trout, Oncochrychus mykiss.";
RL Submitted (DEC-1999) to Swiss-Prote.
CC -1- FUNCTION: Antibacterial activity against Gram-negative bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma serum.
KW Antibiotic.
FT NON TER 13
SQ SEQUENCE 13 AA; 1400 MW; 5FEB792ABE5873 CRC64;

Query Match 32.0%; Score 16; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PWIOG 6
Db 3 FVLKG 7

RESULT 28
LPM_ECOLI STANDARD; PRT; 14 AA.
ID LPM_ECOLI
AC P03053;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Trp operon leader peptide.
GN TRP_Operon TRPEB OR B1265 OR C5494 OR Z2545 OR ECG1837 OR SFL1268 OR
GN S4805.
OS Escherichia coli,
OS Escherichia coli O6,
OS Escherichia coli O157:H7, and
OS Shigella flexneri.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=82150258; PubMed=7038627;
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.B.,
RA Horowitz H., Van Cleemput M., Wu A.W.;
RT "The complete nucleotide sequence of the tryptophan operon of
RT Escherichia coli.";
RL Nucleic Acids Res. 9:6647-6668(1981).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli;
RX MEDLINE=76240562; PubMed=781271;
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RA Yanofsky C.;
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
RT Escherichia coli.";
RL J. Mol. Biol. 103:351-361(1976).
RN [3]
RP SEQUENCE FROM N.A.

RC SPECIES=E.coli;
RX MEDLINE=80101455; PubMed=118451;
RA Oxender D.L., Zurawski G., Yanofsky C.;
RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
RT secondary structure involving the tryptophan codon region.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley W., Coliaco-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:12453-12474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Raeko D.F., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
RT of uropathogenic Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [7]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
RN [8]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
RX MEDLINE=22272406; PubMed=12384590;
RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA Sun L., Xue Y., Zhao X., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA Xu J.;
RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT through comparison with genomes of Escherichia coli K12 and O157.";
RL Nucleic Acids Res. 30:4432-4441(2002).
RN [9]
RP SEQUENCE FROM N.A.
RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX MEDLINE=22590274; PubMed=12704152;
RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA Schwartz D.C., Blattner F.R.;
RT "Complete genome sequence and comparative genomics of Shigella
RT flexneri serotype 2a strain 2457T.";
RL Infect. Immun. 71:2775-2786(2003).

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CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
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 CC -----
 DR EMBL, J01714; AAA57296.1; -;
 DR EMBL, A04494; AAA00361.1; -;
 DR EMBL, AE000224; AAC74347.1; -;
 DR EMBL, AE016760; AAN80196.1; -;
 DR EMBL, AE005380; AAG58580.1; -;
 DR EMBL, AP002556; BAB35260.1; -;
 DR EMBL, AE015153; AAN42881.1; -;
 DR EMBL, AE016982; AAP16766.1; -;
 DR PIR, A03589; LFECEM.
 DR PIR, B85761; B85761.
 DR PIR, B90858; B90858.
 DR Ecogen; B01174; trpL.
 DR Tryptophan biosynthesis; Leader peptide; Complete proteome.
 SQ SEQUENCE 14 AA; 1723 MW; 5B79306E3E804A37 CRC64;
 Query Match 32.0%; Score 16; DB 1; Length 14;
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 2 FMIG 6
 DB 5 FVLKG 9
 RESULT 29
 ACT_THUAL STANDARD; PRT; 8 AA.
 ID ACT_THUAL
 AC P18691;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Angiotensin-converting enzyme inhibitor.
 OS Thunnus albacares (Yellowfin tuna) (Neochannus macropterus).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 CC Acanthomorphi; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
 CC Scombridae; Thunnus.
 OX NCBI_TaxID=8236;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Muscle;
 RX MEDLINE=88326322; PubMed=3415688;
 RA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
 RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
 muscle.";
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
 DR PIR, A31570; A31570.
 SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;
 Query Match 30.0%; Score 15; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 TGGD 8
 DB 4 IKMGD 8
 RESULT 30
 TRNK_PIG STANDARD; PRT; 10 AA.
 ID TRNK_PIG
 AC P01292;

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurokinin B (NKB) (Neuromedin K).
 GN TAC3 OR NKXB.
 OS Sus scrofa (Pig), and
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823, 8406;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Pig; TISSUE=Spinal cord;
 RX MEDLINE=83282812; PubMed=6576785;
 RA Kangawa K., Minamide N., Fukuda A., Matsuo H.;
 RT "Neuromedin K: a novel mammalian tachykinin identified in porcine
 RT spinal cord.";
 RL Biochem. Biophys. Res. Commun. 114:533-540(1983).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=R. ridibunda; TISSUE=Brain;
 RX MEDLINE=92044543; PubMed=1658233;
 RA O'Harte F., Butcher E., Lomas S., Smith D.D., Vaudry H., Conlon J.M.;
 RT "Neurokinin B: a novel NK1 tachykinin receptor agonist isolated with
 RT neurokinin B from the brain of the frog Rana ridibunda.";
 RL J. Neurochem. 57:2086-2091(1991).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 CC evoke behavioral responses, are potent vasodilators and
 CC secretagogues, and contract (directly or indirectly) many smooth
 CC muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A01560; SPGKNK.
 DR InterPro; IPR002040; Tachy_Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KM Tachykinin; Neuropeptide; Amidation.
 PT MOD_RES 10 10
 SQ SEQUENCE 10 AA; 1211 MW; E1FAVC62C9C9CA11 CRC64;
 Query Match 30.0%; Score 15; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.8e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DFMT 4
 DB 4 DFV 7
 RESULT 31
 GER2_HORVU STANDARD; PRT; 13 AA.
 ID GER2_HORVU
 AC P28526;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Germin G82 (Fragment).
 OS Hordeum vulgare (Barley).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 CC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. CM 72; TISSUE=Root;
 RA Hurkman W.U., Tao H.P., Tanaka C.K.;
 RT "Germin-like polypeptides increase in barley roots during salt
 RT stress.";
 RL Plant Physiol. 97:366-374(1991).
 CC -1- FUNCTION: May play a role in altering the properties of cell walls
 CC during germinative growth.
 CC -1- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: SOLUBLE, MICROSMAL AND CELL WALL FRACTIONS.

CC -1- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in the
 CC mature region, but not in the tip. Not detected in leaves.
 CC -1- INDUCTION: Increased by salt stress in roots and decreased by salt
 CC stress in coleoptile.
 CC -1- PTM: Glycosylated.
 CC -1- SIMILARITY: Belongs to the germin family.
 DR InterPro; IPR001929; Germin.
 DR PROSITE; PS00725; GERMIN, PARTIAL.
 KM Apolipoprotein, Cell wall; Glycoprotein; Multigene family.
 FT UNSURE
 FT NON TER 10 10
 FT 13 13
 SQ SEQUENCE 13 AA; 1484 MW; 43FB4A1AA3B7BD7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPMI 4
 |||
 Db 8 DFCI 11

RESULT 32
 ID UN10_CLOPA STANDARD; PRT; 13 AA.
 AC P81345;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Unknown protein CP 10 from 2D-page (Fragment).
 OS Clostridium pasteurianum.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 CC NCBI_TaxID=1501;
 RN (1)
 RP SEQUENCE.
 RC STRAIN=M5;
 RX MEDLINE=96291870; PubMed=962918;
 RA Flensburg R., Skjeldal L.;
 RT "Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from Clostridium pasteurianum M5.";
 RL Electrophoresis 19:802-806(1998).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.2, ITS MW IS: 52.5 Kda.
 CC NON TER 13 13
 CC FT 13 13
 SQ SEQUENCE 13 AA; 1447 MW; ABBE730C4B9C056 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPMI 4
 |||
 Db 4 DIMI 7

RESULT 33
 ID UN10_CITFR STANDARD; PRT; 14 AA.
 AC P03056;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE Trp operon leader peptide.
 GN TRPL.
 OS Citrobacter freundii.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Citrobacter.
 CC NCBI_TaxID=546;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83007061; PubMed=6749821;
 RA Blumenberg M., Yanofsky C.;

RT "Evolutionary divergence of the Citrobacter freundii tryptophan
 RT operon regulatory region: comparison with other enteric bacteria.";
 RL J. Bacteriol. 152:57-62(1982).
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 CC -----
 DR EMBL; U01557; -; NOT ANNOTATED_CDS.
 DR PIR; A03592; LFEHWC.
 KM Tryptophan biosynthesis; Leader peptide.
 SQ SEQUENCE 14 AA; 1720 MW; 5B792A473B8048E7 CRC64;

Query Match 30.0%; Score 15; DB 1; Length 14;
 Best Local Similarity 40.0%; Pred. No. 5.3e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIOG 6
 |||
 Db 5 FVLHG 9

RESULT 34
 ID AL16_CARMA STANDARD; PRT; 8 AA.
 AC P81819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 16.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunidea; Portunidae; Carcinus.
 CC NCBI_TaxID=6759;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 CC Neuropeptide; Amidation; Multigene family.
 CC MOD RES 8 8
 CC FT 8 8
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45B3476878 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 GGDF 9
 |||
 Db 1 GGPV 4

RESULT 35
 ID AL19_CARMA STANDARD; PRT; 8 AA.
 AC P81812;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 9.

```

OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;

RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -1- SIMILARITY: Belongs to the allatostatin family.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 8
SQ SEQUENCE 8 AA; 781 MW; 7C2679CDB476878 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 GQDF 9
DB 1 GSPY 4

RESULT 36
CCCN MACCU STANDARD; PRT; 8 AA.
AC P30359;
AC 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cholecystokinin (CCK).
GN CCK.
OS Macropus eugenii (Tamar wallaby), and
OS Dasyurus viverrinus (Southeastern quoll).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315, 9279;
RN [1]
RP SEQUENCE.
RC SPECIES=M. eugenii, and D. viverrinus;
RC TISSUE=Brain;
RX MEDLINE=88234141; PubMed=3375140;
RA Pan Z.W., Eng C., Shaw G., Yalow R.S.;
RT "Cholecystokinin octapeptide purified from brains of Australian
RT marsupials.";
RL Peptides 9:429-431(1988).
CC -1- FUNCTION: This peptide hormone induces gall bladder contraction
CC and the release of pancreatic enzymes in the gut. Its function in
CC the brain is not clear.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC CC
CC PIR; A43001; A43001.
DR PIR; PQ0012; PQ0012.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Sulfation; Hormone.
FT MOD_RES 2
FT MOD_RES 8
FT MOD_RES 8
SQ SEQUENCE 8 AA; 1064 MW; DDCAA68378768B5A CRC64;

Query Match 28.0%; Score 14; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.4e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
DB 1 DYM 3

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RESULT 37
AMPN HELAM STANDARD; PRT; 10 AA.
ID AMPN HELAM
AC P81731;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Aminopeptidase N (EC 3.4.11.2) (CRYIA(C) receptor) (Fragment).
OS Helicoverpa armigera (Cotton bollworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryia; Noctuoidea;
OC Noctuidae; Heliothinae; Helicoverpa.
OX NCBI_TaxID=29058;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RA Ingle S.S., Trivedi N., Praead R., Rao K.K., Chatpar H.S.;
RT "Aminopeptidase-N as a receptor for Bacillus thuringiensis CryIc
RT toxin from Helicoverpa armigera.";
RL Submitted (MAR-1999) to Swiss-Prot.
CC -1- FUNCTION: ACTS AS A RECEPTOR FOR B.THURINGIENSIS TOXIN CRYIAC.
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal amino acid, Xaa-
CC Xbb- from a peptide, amide or arylamide. Xaa is preferably Ala,
CC but may be most amino acids including Pro (slow action). When a
CC terminal hydrophobic residue is followed by a prolyl residue, the
CC two may be released as an intact Xaa-Pro dipeptide.
CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family M1.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR PROSITE; PS00142; ZINC_PROTEASE; PARTIAL.
KM Hydrolase; Metalloprotease; Aminopeptidase; Zinc.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1093 MW; 05042EB87B1F1FB CRC64;

Query Match 28.0%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GQGD 8
DB 6 EGSD 9

RESULT 38
Q2OG COMTE STANDARD; PRT; 10 AA.
ID Q2OG COMTE
AC B80456;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinolone 2-oxidoeductase, gamma chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Comamonadaceae; Comamonas.
OX NCBI_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Teshitaka B., Feltzer S., Lingens F.;
RT "Quinolone 2-oxidoeductase and 2-oxo-1,2-dihydroquinoline 5,6-
RT dioxygenase from Comamonas testosteroni 63. The first two enzymes in
RT quinoline and 3-methylquinoline degradation.";
RL Eur. J. Biochem. 232:536-544(1995).
CC -1- FUNCTION: Converts (3-methyl-)-quinoline to (3-methyl-)-2-oxo-1,2-
CC dihydroquinoline.
CC -1- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = isoguinolin-
CC 1(2H)-one + reduced acceptor.
CC -1- COFACTOR: FAD, molybdenum and iron-sulfur.
CC -1- PATHWAY: Degradation of quinoline and (3-methyl-)-quinoline, first
CC step.
CC -1- SUBUNIT: Heterohexamer of two alpha chains, two beta chains, and

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CC      two gamma chains (Probable).
KW      Oxidoreductase; Flavoprotein; FAD; Molybdenum.
FT      NON TER
SQ      SEQUENCE 10 AA; 1153 MW; C848CE64433B1DC6 CRC64;

Query Match
Best Local Similarity 28.0%; Score 14; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 MIQ 5
        |||
Db       1 MIQ 3

RESULT 39
TPIS_NICPL STANDARD; PRT; 10 AA.
ID TPIS_NICPL
AC P1918;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).
OS Nicotiana glauca (L.) Wieg. & Griseb. (Leadwort-leaved tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Nicotiana.
OX NCBI_Taxid=4092;
RN [1]
RP SEQUENCE.
RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electrophoretically separated from two-
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glyceralone
CC phosphate.
CC -1- PATHWAY: Plays an important role in several metabolic pathways.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- MISCELLANEOUS: In plants, there are two types of TPIS, cytosolic
CC and plastid.
CC -1- SIMILARITY: Belongs to the triosephosphate isomerase family.
DR PIR: A27617; A27617.
DR InterPro: IPR000652; Triophos_ismrse.
DR PROSITE: PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON TER
SQ SEQUENCE 10 AA; 1140 MW; 80B9D378629C9D1 CRC64;

Query Match
Best Local Similarity 28.0%; Score 14; DB 1; Length 10;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      6 GQDF 9
        |||
Db       7 GGNW 10

RESULT 40
PKC1_CARMO STANDARD; PRT; 11 AA.
ID PKC1_CARMO
AC P82684;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Pyrokinin-1 (Cam-PK-1) (FXPR1-Amide).
OS Carusius morosus (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Phasmatodea; Euphasmatida; Phasmatodea;
OC Heteromulidae; Carausius.
OX NCBI_Taxid=7022;
RN [1]

```

```

RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=Corpora cardiaca;
RA Predele R., Kellner R., Gaede G.;
RT "Myotropic peptides from the retrocerebral complex of the stick
RT insect, Carusius morosus (Phasmatodea: Lonchodidae).";
RL Eur. J. Entomol. 96:275-278(1999).
CC -1- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC activity).
CC -1- MASS SPECTROMETRY: MW=1235; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the pyrokinin family.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; FALSE NEG.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES
SQ SEQUENCE 11 AA; 1236 MW; 2BFA5225BB46C1A8 CRC64;

Query Match
Best Local Similarity 28.0%; Score 14; DB 1; Length 11;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 QGG 7
        |||
Db       2 EGG 4

RESULT 41
CRBL_VESTR STANDARD; PRT; 13 AA.
ID CRBL_VESTR
AC P17231;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vespid chemotactic peptide T (VZSCP-T).
OS Vespa tropica (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_Taxid=7450;
RN [1]
RP SEQUENCE.
RA TISSUE=Venom;
RA Yasuhara T., Nakajima T., Erspamer V.;
RL (in) Sakakibara S. (eds.);
RL Peptide chemistry 1982, pp.213-218, Protein Research Foundation,
RL Osaka (1983).
CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
CC of neutrophils.
KW Mast cell degranulation; Chemotaxis; Amidation.
FT MOD_RES
SQ SEQUENCE 13 AA; 1354 MW; 220140365DFE5338 CRC64;

Query Match
Best Local Similarity 28.0%; Score 14; DB 1; Length 13;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      4 IQGG 7
        |||
Db       8 ILGG 11

RESULT 42
GER1_HORVU STANDARD; PRT; 13 AA.
ID GER1_HORVU
AC P28525;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Germin GSI (Fragment).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_Taxid=4513;
RN [1]

```

RN (1)
 RP SEQUENCE.
 RC STRAIN=cv. CM 72; TISSUE=Root;
 RA Hurtman W.J., Tao H.P., Tanaka C.K.;
 RT "Germ-in-like polypeptides increase in barley roots during salt
 stress";
 RL Plant Physiol. 97:366-374(1991).
 CC -1- FUNCTION: May play a role in altering the properties of cell
 walls during germinative growth.
 CC -1- SUBUNIT: Oligomer (believed to be a pentamer but probably hexamer)
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: SOLUBLE, MICROSOMAL AND CELL WALL FRACTIONS.
 CC -1- TISSUE SPECIFICITY: Roots and coleoptile. In roots, present in
 the mature region, but not in the tip. Not detected in leaves.
 CC -1- INDUCTION: Increased by salt stress in roots and decreased by salt
 stress in coleoptile.
 CC -1- PTM: Glycosylated.
 CC -1- SIMILARITY: Belongs to the germin family.
 DR InterPro: IPR001929; Germin.
 DR PROSITE: PS00725; GERMIN, PARTIAL.
 KM Apolact, Cell wall; Glycoprotein; Multigene family.
 FT UNSURE
 FT NON TER
 FT 10
 SQ SEQUENCE 13 AA; 1470 MW; 43FB588AA3B7BD7 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 7.7e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPMI 4
 DB 8 DPCV 11

RESULT 43
 NP3_LYMST STANDARD; PRT; 13 AA.
 AC P80180;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE Lymnaea-DF-amide 3.
 DE Lymnaea stagnalis (Great pond snail).
 OS Lymnaea stagnalis (great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Bascommatophora;
 CC Lymnaeidae; Lymnaeidae; Lymnaea.
 OX NCBI_TaxId=6523;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Ganglion;
 RX MEDLINE=93238777; PubMed=8477756;
 RA Johnson A.H., Rehfeld J.F.;
 RT "Lymnaeidae, a new family of neuropeptides from the pond snail,
 Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
 invertebrates";
 RL Eur. J. Biochem. 213:875-879(1993).
 CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CKK) FAMILY.
 DR PIR, S32473; S32473.
 KW Neuropeptide; Amidation.
 FT MOD RES
 FT 13
 FT 12
 FT 12
 FT UNSURE
 FT 13
 SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 7.7e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 IOGDF 9
 DB 5 ISGANF 10

RESULT 44
 TAL3_TREME

ID TAL3_TREME STANDARD; PRT; 13 AA.
 AC P01370;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tremorgen A-13.
 OS Tremella mesenterica (Veily fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 CC Tremellomycetidae; Tremellales; Tremellaceae; Tremella.
 OX NCBI_TaxId=5217;
 RN [1]
 RP SEQUENCE.
 RA Sakagami Y., Yoshida M., Isogai A., Suzuki A.;
 RT "Peptide sex hormones inducing conjugation tube formation in
 compatible mating-type cells of Tremella mesenterica";
 RL Science 212:1525-1527(1981).
 CC -1- FUNCTION: Tremorgen A-13 is produced by the a mating-type cells
 and induces formation of conjugation tubes in a mating-type cells.
 DR PIR: A01641; J0033.
 KM Lipoprotein; Prenylation; Pheromone.
 FT LIPID
 FT 13
 FT 13
 SQ SEQUENCE 13 AA; 1204 MW; 680304A9697BA864 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 7.7e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 OGG 7
 DB 1 EGG 3

RESULT 45
 COCO_LIMPO STANDARD; PRT; 14 AA.
 AC P35586;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cocoonase (EC 3.4.21.-) (Fragment).
 OS Limulus polyphemus (Atlantic horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 CC Limulidae; Limulus.
 OX NCBI_TaxId=6850;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78037243; PubMed=335821;
 RA Iaw J.H., Dunn P.E., Kramer K.J.;
 RT "Insect proteases and peptidases";
 RL Adv. Enzymol. Relat. Areas Mol. Biol. 45:389-425(1977).
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-, Lys-,
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- SIMILARITY: Belongs to peptidase family S1.
 DR MEROPS: S01.112; -.
 DR InterPro: IPR001254; peptidase_S1.
 DR PROSITE: PS50240; TRYPSIN_DOM; PARTIAL.
 DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
 DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
 KM Hydrolyase; Serine protease.
 FT NON TER
 FT 14
 FT 14
 SQ SEQUENCE 14 AA; 1452 MW; 1615FB1D73747570 CRC64;

Query Match 28.0%; Score 14; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 IOGG 7
 DB 1 IVGG 4

Search completed: August 30, 2004, 10:50:18
 Job time : 3.55068 secs

Thu Sep 2 07:41:32 2004

us-09-720-469a-2.aug30.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:41:54 ; Search time 2.70608 Seconds
(without alignments)
319.918 Million cell updates/sec

Title: US-09-720-469A-2
Perfect score: 50
Sequence: 1 DPMIOGDPF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1638

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR78:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	52.0	11	2 B60769	Ig H2 chain - Paci
2	24	48.0	14	2 PH0945	T-cell receptor be
3	23	46.0	12	2 A61309	glycoprotein hor
4	23	46.0	13	2 PH1585	Ig H chain V-D-J r
5	22	44.0	14	2 S23376	collagen alpha cha
6	20	40.0	12	2 S43170	kinasin light chai
7	20	40.0	12	2 PH1458	T-cell receptor be
8	19	38.0	10	2 C60787	sperm-activating p
9	19	38.0	10	2 C60527	sperm-activating p
10	19	38.0	10	2 E39572	sperm-activating p
11	19	38.0	10	2 D60589	sperm-activating p
12	19	38.0	10	2 A60588	sperm-activating p
13	19	38.0	10	2 PNO165	triase-phosphate i
14	19	38.0	11	2 PU0029	33k protein 3218 -
15	19	38.0	14	2 S72217	D-arabinose 1-dely
16	18	36.0	9	2 USG318	leucokinin VIII -
17	18	36.0	9	2 QDRB	delta sleep-induci
18	18	36.0	10	2 G60527	sperm-activating p
19	18	36.0	10	2 F60589	sperm-activating p
20	18	36.0	11	2 PTO250	Ig heavy chain CbD
21	18	36.0	11	2 PH1343	Ig heavy chain Df
22	18	36.0	11	2 S60354	retinal oxidase -
23	18	36.0	11	2 PNO044	protein kinase C i
24	18	36.0	11	2 PTO218	T-cell receptor be
25	18	36.0	11	2 I41946	T-cell receptor ga
26	18	36.0	11	2 A61575	Trimeresurus serin
27	18	36.0	12	2 S26544	T-cell receptor be
28	18	36.0	13	2 S48210	collagen alpha 1(V
29	18	36.0	14	2 PS0278	ribulose-bisphosph

30	18	36.0	14	2 E33098	214k exoantigen (v
31	18	36.0	14	2 PH1347	Ig heavy chain Df
32	18	36.0	14	2 PH1598	Ig H chain V-D-J r
33	17	34.0	8	2 A41978	calliFMRamide 8 -
34	17	34.0	9	1 YFPG	thymic factor - p1
35	17	34.0	9	2 A60857	thymocyte growth p
36	17	34.0	9	2 A41978	calliFMRamide 1 -
37	17	34.0	9	2 A44787	calliFMRamide 10
38	17	34.0	9	2 B41978	calliFMRamide 2 -
39	17	34.0	9	2 C41978	calliFMRamide 3 -
40	17	34.0	9	2 D41978	calliFMRamide 4 -
41	17	34.0	9	2 E41978	calliFMRamide 5 -
42	17	34.0	9	2 F41978	calliFMRamide 6 -
43	17	34.0	9	2 G41978	calliFMRamide 7 -
44	17	34.0	10	2 F60787	sperm-activating p
45	17	34.0	10	2 E60788	sperm-activating p

ALIGNMENTS

RESULT 1
B60769
Ig H2 chain - Pacific hagfish (fragment)
C:Species: Epratreus scouti (Pacific hagfish)
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 03-Jun-1993
C:Accession: B60769
R:Hanley, P.J.; Seppelt, I.M.; Gookey, A.A.; Hook, J.W.; Ralson, R.L.
J. Immunol. 145, 3823-3828, 1990
A:Title: Distinct Ig H chains in a primitive vertebrate, Epratreus scouti.
A:Reference number: A60769; UID:91060965; PMID:2123225
A:Accession: B60769
A:Status: preliminary
A:Molecule type: Protein
A:Residues: 1-11 <HAN>

Query Match 52.0%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPMIO 5
DB 5 DPMIO 9

RESULT 2
PH0945
T-cell receptor beta chain V-D-J region (clone 16) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0945
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy:
A:Reference number: PH0945; UID:92078857; PMID:1836012
A:Molecule type: mRNA
A:Residues: 1-14 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A>Note: the authors translated the codon TTC for residue 11 as Ser
C:Keywords: T-cell receptor

Query Match 48.0%; Score 24; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGDF 9
DB 8 GGDF 11

RESULT 3
A61309

glycoprotein hormones alpha chain - hamster (fragment)
 NAlternate names: chorionadotropin alpha chain; luteinizing hormone alpha chain; lut
 C/Species: Cricetinae gen. sp. (hamster)
 C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C/Accession: A61309
 R/Glen, S.D.; Nahm, H.S.; Greenwald, G.S.; Ward, D.N.
 Endocrinology 111, 1263-1269, 1992
 A/Title: Isolation and characterization of hamster luteinizing hormone.
 A/Reference number: A61309; PMID:83003498; PMID:6889489
 A/Accession: A61309
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-112 <GIE>
 C/Superfamily: glycoprotein hormones alpha chain
 C/Keywords: glycoprotein

Query Match 46.0%; Score 23; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DMIOG 6
 ||:|
 DB 5 DFTMOG 10

RESULT 4
 PH1585
 Ig H chain V-D-J region (wild-type clone 9) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1585
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A/Reference number: PH1580; PMID:93301609; PMID:8315387
 A/Accession: PH1585
 A/Molecule type: DNA
 A/Residues: 1-13 <LEV>
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 46.0%; Score 23; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 OGDF 9
 ||:|
 DB 5 EGGDY 9

RESULT 5
 S23376
 collagen alpha chain - polychaete (Alvinella pompejana) (fragment)
 C/Species: Alvinella pompejana
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 29-May-1998
 C/Accession: S23376
 R/Gail, F.; Wiedemann, H.; Mann, K.; Kuehn, K.; Timpl, R.; Engel, J.
 J. Mol. Biol. 221, 209-223, 1991
 A/Title: Molecular characterization of cuticle and interstitial collagens from worms col
 A/Reference number: S17581; PMID:92015209; PMID:1920405
 A/Accession: S23376
 A/Molecule type: protein
 A/Residues: 1-14 <GAT>

Query Match 44.0%; Score 22; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2.9e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOG 7
 ||:|
 DB 1 FOAGG 6

RESULT 6
 S43170
 kinesin light chain - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
 C/Accession: S43170
 R/Cernakovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
 Submitted to the EMBL Data Library, December 1992
 A/Description: Promoter first exon/intron characterization and chromosomal location of th
 A/Reference number: S43170
 A/Accession: S43170
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-112 <CHB>
 A/Cross-references: EMBL:X69658; NID:g468786; PIDN:CAA49349.1; PID:g468787

Query Match 40.0%; Score 20; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 6.3e+02;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOG 7
 ||:|
 DB 1 MROG 5

RESULT 7
 PH1458
 T-cell receptor beta chain (clone 332/1K) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 17-Mar-1999
 C/Accession: PH1458; S26543
 R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kov
 J. Exp. Med. 177, 811-820, 1993
 A/Title: T cell receptor selection by and recognition of two class I major histocompatib
 A/Reference number: PH1430; PMID:93171821; PMID:8436911
 A/Accession: PH1458
 A/Molecule type: mRNA
 A/Residues: 1-112 <CAS>
 A/Experimental source: cytoytic T-lymphocyte, clone 332/1K
 R/Casanova, J.L.; Gerotini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A/Title: H-2-restricted cytoytic T lymphocytes specific for HLA display T cell receptor
 A/Reference number: S26512; PMID:92364546; PMID:1380061
 A/Accession: S26543
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-112 <CA2>
 A/Cross-references: EMBL:X67993
 A/Experimental source: cytoytic T-lymphocyte, clone Cw3/C44
 C/Superfamily: immunoglobulin homology
 C/Keywords: receptor; T-cell

Query Match 40.0%; Score 20; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 6.3e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 OGDF 9
 ||:|
 DB 5 EGGDY 9

RESULT 8
 C60787
 sperm-activating peptide (Ser-3,10 speract) - sea urchin (Hemicentrotus pulcherrimus)
 C/Species: Hemicentrotus pulcherrimus
 C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
 C/Accession: C60787
 R/Suzuki, N.; Kajihara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H
 Comp. Biochem. Physiol. B 89, 687-693, 1998
 A/Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrot
 A/Reference number: A60787; PMID:88242184; PMID:13378407
 A/Accession: C60787
 A/Molecule type: protein

A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
| : |||
Db 2 FSLSGG 7

RESULT 9

sperm-activating peptide (Ser-3, Ile-4, Gly-5 SAp-I) - sea urchin (*Tripleneustes gratillia*)
N:Alternate names: speract homolog TG-4
C:Species: *Tripleneustes gratillia*
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: C60527; D39572
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi,
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, *Echinometra mathaei* and *Heterocentrotus mammillatus*.
A:Reference number: A60527
A:Accession: C60527
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A>Note: this peptide did not contain bromophenylalanine

R:Yoshino, K.; Takao, T.; Subara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh
Biochemistry 30, 6203-6209, 1991
A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
A:Reference number: A39572; PMID:2059627
C:Accession: D39572
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A>Note: this peptide contained bromophenylalanine
C:Superfamily: unassigned animal peptides
C:Keywords: bromine
F:2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
| : |||
Db 2 FSLSGG 7

RESULT 10

E39572
sperm-activating peptide TG-5 - sea urchin (*Tripleneustes gratillia*)
N:Alternate names: speract homolog TG-5
C:Species: *Tripleneustes gratillia*

C>Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 18-Aug-2000
C:Accession: E39572

R:Yoshino, K.; Takao, T.; Subara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh
Biochemistry 30, 6203-6209, 1991
A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associate
A:Reference number: A39572; PMID:2059627
C:Accession: E39572
A:Molecule type: protein
A:Residues: 1-10 <YOS>
C:Superfamily: unassigned animal peptides
C:Keywords: bromine
F:2/Modified site: 2'-bromophenylalanine (Phe) #status experimental

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
| : |||
Db 2 FSLSGG 7

RESULT 11

D60589
sperm-activating peptide (Ser-3,5 SAp-I) - *Echinometra mathaei*
C:Species: *Echinometra mathaei*
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: D60589
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi,
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, *Echinometra mathaei* and *Heterocentrotus mammillatus*.
A:Reference number: A60527
A:Accession: D60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A>Note: an identical peptide was isolated from *Echinometra mathaei* type A and type B
C:Superfamily: unassigned animal peptides

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
| : |||
Db 2 FSLSGG 7

RESULT 12

A60588
sperm-activating peptide (Ser-3,5 SAp-I) - sea urchin (*Strongylocentrotus nudus*)
N:Alternate names: speract homolog
C:Species: *Strongylocentrotus nudus*
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60588
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi,
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, *Echinometra mathaei* and *Heterocentrotus mammillatus*.
A:Reference number: A60527
A:Accession: A60588
A:Molecule type: protein
A:Residues: 1-10 <YOS>
C:Superfamily: unassigned animal peptides

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
| : |||
Db 2 FSLSGG 7

RESULT 13

FN0165
triose-phosphate isomerase (EC 5.3.1.1) - fungus (*Fusarium sporotrichioides*) (fragment)
C:Species: *Fusarium sporotrichioides*
C>Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: FN0165
R:Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JIPID, May 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of *Fusarium sporotrichi*
A:Reference number: FN0160
A:Accession: FN0165
A:Molecule type: protein
A:Residues: 1-10 <FKU>
A:Experimental source: strain M-1-1
C:Keywords: intramolecular oxidoreductase; isomerase

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query Match 38.0%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.3e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGGP 9
DB 7 GGNF 10

RESULT 14

P00029

33k protein 3218 - rice (strain Nohohbare) (fragment)

C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C:Accession: P00029

R:Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993

A:Reference number: P50208

A:Accession: P00029

A:Molecule type: protein

A:Residues: 1-11 <TSU>

A:Experimental source: brain

C:Comment: molecular weight 33K, pI 6.0.

Query Match 38.0%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 9.2e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGP 9
DB 3 EGGPF 7

RESULT 15

S72217

D-arabinose 1-dehydrogenase [NAD(P)] (EC 1.1.1.117) - yeast (Candida albicans) (fragment)

C:Species: Candida albicans

C>Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 03-Jun-2002

C:Accession: S72217

R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.

Biochim. Biophys. Acta 1297, 1-8, 1996

A:Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in Candida a

A:Reference number: S72217; PMID:96439039; PMID:8841374

A:Accession: S72217

A:Molecule type: protein

A:Residues: 1-14 <KIM>

C:Keywords: oxidoreductase

Query Match 38.0%; Score 19; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DFMIQGG 7
DB 8 DFXLNNG 14

RESULT 16

J50318

leucokinin VIII - Madeira cockroach

C:Species: Leucophaea madeira (Madeira cockroach)

C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000

C:Accession: J50318

R:Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 31-34, 1987

A:Title: Isolation, primary structure and synthesis of leucokinin VII and VIII: the fin

A:Reference number: J50317

A:Accession: J50318

A:Molecule type: protein

A:Residues: 1-8 <HOL>
C:Comment: leucokinin, a family of cephalomyotropic peptides, stimulate contractile act
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F/8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 36.0%; Score 18; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGGP 9
DB 1 GADF 4

RESULT 17

QDRB

delta sleep-inducing peptide - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C>Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000

C:Accession: A01422

R:Monnier, M.; Dudler, L.; Gachter, R.; Mater, P.F.; Tobler, H.J.; Schoenenberger, G.A.

Experientia 33, 548-552, 1977

A:Title: The delta sleep inducing peptide (DSIP). Comparative properties of the original

A:Reference number: A01422; PMID:77185324; PMID:862769

A:Accession: A01422

A:Molecule type: protein

A:Residues: 1-9 <MON>

C:Comment: This peptide was obtained from dialysates of occipital venous sinus blood from

C:Superfamily: unassigned animal peptides

Query Match 36.0%; Score 18; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
DB 3 GGD 5

RESULT 18

G60527

sperm-activating peptide (Br-Phe-2, Asn-3 SAP-I) - sea urchin (Tripneustes gratilla)

N:Alternate names: speract homolog TG-2; TG-10

C:Species: Tripneustes gratilla

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000

C:Accession: G60527; B39572; A40051; B60527

R:Yoshino, K.; Takao, T.; Shihara, M.; Kitta, T.; Hori, H.; Nomura, K.; Yamaguchi, M.

Comp. Biochem. Physiol. B 94, 739-751, 1989

A:Title: A halogenated amino acid-containing sperm activating peptide and its related pep

A:Reference number: A60527

A:Accession: G60527

A:Molecule type: protein

A:Residues: 1-10 <YOS>

A:Note: this peptide was found both with both phenylalanine and bromophenylalanine

R:Yoshino, K.; Takao, T.; Shihara, M.; Kitta, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh

Biochemistry 30, 6203-6209, 1991

A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated

A:Reference number: A39572; PMID:91283461; PMID:2059627

A:Accession: B39572

A:Molecule type: protein

A:Residues: 1-10 <YOS>

C:Superfamily: unassigned animal peptides

C:Keywords: bromine

F/2/Modified site: 2'-bromophenylalanine or 4'-bromophenylalanine (Phe) (partial) #status

Query Match 36.0%; Score 18; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
DB 2 FMIOGG 7

RESULT 19

FE0589
 sperm-activating peptide (Asn-3, Ser-5 SGP-I) - Echinosmetra mathaei (type A)
 C/Species: Echinosmetra mathaei
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
 C/Accession: FE0589
 R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, K.
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptides
 A/Reference number: A60527
 A/Accession: FE0589
 A/Molecule type: protein
 A/Residues: 1-10 <YOS>
 C/Superfamily: unassigned animal peptides

Query Match 36.0%; Score 18; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.3e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
 |||
 Db 2 FNLSCG 7

RESULT 20

PT0250
 Ig heavy chain CRD3 region (clone 2-109B) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0250
 R/Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0250
 A/Molecule type: DNA
 A/Residues: 1-11 <YAM>
 A/Experimental source: B lymphocyte
 C/Keywords: heterodimer; immunoglobulin

Query Match 36.0%; Score 18; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GDF 9
 |||
 Db 4 GDF 6

RESULT 21

PH1343
 Ig heavy chain DJ region (clone C100-91) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: PH1343
 R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A/Reference number: PH1302; MUID:93094761; PMID:1460419
 A/Accession: PH1343
 A/Molecule type: DNA
 A/Residues: 1-11 <WAS>
 C/Keywords: heterodimer; immunoglobulin

Query Match 36.0%; Score 18; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
 |||
 Db 1 GGD 3

RESULT 22

S60354
 retinal oxidase - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C/Accession: S60354
 R/Huang, D.Y.; Ichikawa, Y.
 Biochim. Biophys. Acta 1243, 431-436, 1995
 A/Title: Identification of essential [lysyl] and cysteinyl residues, and the amino acid se
 A/Reference number: S60354; MUID:95244596; PMID:7727518
 A/Accession: S60354
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-11 <HUA>

Query Match 36.0%; Score 18; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
 |||
 Db 1 GGD 3

RESULT 23

PN0044
 protein kinase C inhibitor I - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
 C/Accession: PN0044
 R/Kato, H.
 Kawasaki, Igakaishi 22, 245-259, 1996
 A/Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuro
 A/Reference number: PN0041
 A/Accession: PN0044
 A/Molecule type: protein
 A/Residues: 1-11 <KAT>
 A/Experimental source: neuroblastoma cell
 C/Comment: The molecular mass is 13,900 and the pI is 6.36. The amino-terminus is blocke
 C/Keywords: brain

Query Match 36.0%; Score 18; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
 |||
 Db 8 GGD 10

RESULT 24

PT0218
 T-cell receptor beta chain V-J region (7-10-D.3) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
 C/Accession: PT0218
 R/Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
 J. Exp. Med. 173, 1091-1097, 1991
 A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restrict
 A/Reference number: PT0209; MUID:91217621; PMID:11902501
 A/Accession: PT0218
 A/Molecule type: mRNA
 A/Residues: 1-11 <NAK>
 C/Keywords: T-cell receptor

Query Match 36.0%; Score 18; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.5e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 OGGD 8
 |||
 Db 5 OGGN 8

RESULT 25

141946

T-cell receptor gamma chain (5c.1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

C/Accession: I41946

R/Whetzel, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.

Mol. Cell. Biol. 11, 5902-5909, 1991

A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene

A/Reference number: A41946; MUID:92049316; PMID:1658619

A/Accession: I41946

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: DNA

A/Residues: 1-11 <WHB>

C/Keywords: T-cell receptor

Query Match 36.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
Db 5 GGD 7

RESULT 26

A61575

Trimeresurus serine proteinase (EC 3.4.21.-) - Sakishima habu (fragment)

M/Alternate names: hemorrhagic toxin

C/Species: Trimeresurus elegans (Sakishima habu)

C/Date: 20-Oct-1994 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: A61575

R/Nikai, T.; Komori, Y.; Imai, K.; Sugihara, H.

Int. J. Biochem. 23, 73-78, 1991

A/Title: Isolation and characterization of hemorrhagic toxin from the venom of Trimeresurus

A/Reference number: A61575; MUID:91216327; PMID:2022298

A/Accession: A61575

A/Molecule type: protein

A/Residues: 1-11 <NIK>

C/Keywords: hydrolase; serine proteinase; venom

Query Match 36.0%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
Db 3 GGD 5

RESULT 27

S26544

T-cell receptor beta chain (clone Cw3/HLAIC8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C/Accession: S26544

R/Casanova, U.L.; Cerotini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26544

A/Molecule type: mRNA

A/Residues: 1-12 <CAS>

A/Cross-references: EMBL:X67994

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/HLAIC8

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 36.0%; Score 18; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 QGGDF 9
|||
Db 5 QGTDY 9

RESULT 28

S48210

collagen alpha 1(V) chain - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 15-Jul-1995 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C/Accession: S48210

R/Niyibizi, C.; Eyre, D.R.

Eur. J. Biochem. 224, 943-950, 1994

A/Title: Structural characteristics of cross-linking sites in type V collagen of bone. C

A/Reference number: S48210; MUID:95010086; PMID:7925418

A/Accession: S48210

A/Molecule type: protein

A/Residues: 1-13 <NIY>

C/Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology

Query Match 36.0%; Score 18; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
Db 7 GGD 9

RESULT 29

PS0278

ribulose-bisphosphate carboxylase activase I - rice (strain Nihonbare) (fragment)

C/Species: Oryza sativa (rice)

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 02-Jul-1998

C/Accession: PS0278

R/Ishigita, A.

submitted to JIPID, April 1993

A/Reference number: PS0206

A/Accession: PS0278

A/Molecule type: protein

A/Residues: 1-14 <ISH>

Query Match 36.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GDF 9
|||
Db 6 GDF 8

RESULT 30

E33098

21kD exoantigen (version 2) - malaria parasite (Plasmodium falciparum) (fragments)

C/Species: Plasmodium falciparum

C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C/Accession: E33098

R/Nichols, J.H.; Hager, L.P.

submitted to the Protein Sequence Database, May 1990

A/Reference number: A33098

A/Accession: E33098

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <NIC>

Query Match 36.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||

Db 3 GGD 5

RESULT 31

PH1347
Ig heavy chain DJ region (clone C100-103A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1347
R/Maserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DH joining in young children with B precursor lymph
A/Reference number: PH1302; PMID:9309461; PMID:1460419
A/Accession: PH1347
A/Molecule type: DNA
A/Residues: 1-14 <WAS>
C/Keywords: heterotrimer; immunoglobulin

Query Match 36.0%; Score 18; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFMIG 6
|||
Db 5 DFLTNG 10

RESULT 32

PH1598
Ig H chain V-D-J region (wild-type clone 306) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1598
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A/Reference number: PH1580; PMID:93301609; PMID:8315387
A/Accession: PH1598
A/Molecule type: DNA
A/Residues: 1-14 <LEV>
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 36.0%; Score 18; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGD 8
|||
Db 8 GGD 10

RESULT 33

H41978
Calliphora vomitoria 8 - bluebottle fly (Calliphora vomitoria)
C/Species: Calliphora vomitoria
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C/Accession: H41978
R/Duve, H.; Johnson, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rahfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A/Title: Isolation, structure, and activity of a Phe-Met-Arg-Phe-NH-2 neuropeptides (des)
A/Reference number: H41978; PMID:9219611; PMID:1549595
A/Accession: H41978
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <DUV>
C/Keywords: amidated carboxyl end; neuropeptide
F/8/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 4 DFM 6

RESULT 34

YFPG
thymic factor - pig (facteur thymique serique)
N/Alternate names: FTS (facteur thymique serique)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 07-May-1999
C/Accession: A01523; A60983
R/Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
J. Biol. Chem. 252, 8045-8047, 1977
A/Title: Structural study of circulating thymic factor: a peptide isolated from pig seru
A/Reference number: A01523; PMID:78026571; PMID:914862
A/Accession: A01523
A/Molecule type: protein
A/Residues: 1-9 <PLS>
R/Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A/Title: Biochemical characterisation of a serum thymic factor.
A/Reference number: A60983; PMID:77123829; PMID:300146
A/Accession: A60983
A/Molecule type: protein
A/Residues: 'Z', '2-4', 'Z', '6-9' <BAC>
C/Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C/Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modifica
C/Superfamily: thymic factor
C/Keywords: pyrrolidonic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 34.0%; Score 17; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
|||
Db 5 QGG 7

RESULT 35

A60957
thymocyte growth peptide - sheep
N/Contents: FTS (facteur thymique serique)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
C/Accession: A60957
R/Ernstrem, U.; Gafvelin, G.; Rudja, J.M.
Biosci. Rep. 10, 403-412, 1990
A/Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship
A/Reference number: A60957; PMID:91064427; PMID:2249004
A/Accession: A60957
A/Molecule type: protein
A/Residues: 1-9 <ERN>
C/Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C/Comment: This peptide was isolated in two forms. One form contained the pyrrolidone ca
rboxyl end (thymocyte growth peptide) contains a large, non-peptide blocking group with a hi
C/Superfamily: thymic factor
C/Keywords: blocked amino end; pyrrolidonic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) (in FTS) #status experimental
F/1/Modified site: blocked amino end (Gln) (in thymocyte growth peptide) #status experin

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QGG 7
|||
Db 5 QGG 7

RESULT 36
A41978
callIFMRamide 1 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: A41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; PMID:92196111; PMID:1549595
A:Accession: A41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match
Best Local Similarity 34.0%; Score 17; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 37
A44787
callIFMRamide 10 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: A44787
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; PMID:92196111; PMID:1549595
A:Accession: A44787
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match
Best Local Similarity 34.0%; Score 17; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 38
B41978
callIFMRamide 2 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: B41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; PMID:92196111; PMID:1549595
A:Accession: B41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match
Best Local Similarity 34.0%; Score 17; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 39
C41978
callIFMRamide 3 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: C41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; PMID:92196111; PMID:1549595
A:Accession: C41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match
Best Local Similarity 34.0%; Score 17; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 40
D41978
callIFMRamide 4 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: D41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; PMID:92196111; PMID:1549595
A:Accession: D41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match
Best Local Similarity 34.0%; Score 17; DB 2; Length 9;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 41
E41978
callIFMRamide 5 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: E41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; PMID:92196111; PMID:1549595
A:Accession: E41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide

F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 42

F41978
Calliphoramide 6 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: F41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; MUID:92196111; PMID:1549595
A:Accession: F41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 43

G41978
Calliphoramide 7 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: G41978
R:Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A:Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A:Reference number: A41978; MUID:92196111; PMID:1549595
A:Accession: G41978
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <DUV>
C:Keywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.0%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFM 3
|||
Db 5 DFM 7

RESULT 44

F60787
Sperm-activating peptide (Ser-5 speract) - sea urchin (Anthocidaris crassispina)
C:Species: Anthocidaris crassispina
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 18-Aug-2000
C:Accession: F60787
R:Suzuki, N.; Kajitara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, pseudocentro
A:Reference number: A60787; MUID:88242184; PMID:3378407

A:Accession: F60787

A:Molecule type: protein

A:Residues: 1-10 <SUZ>

C:Comment: This oligopeptide from egg jelly is one of several from this species, all of w
at shows some, but not absolute, species restriction.

C:Superfamily: unassigned animal peptides

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
|:|
Db 2 FDLGG 7

RESULT 45

E60788
Sperm-activating peptide (Ala-3, Gly-5 speract) - sea urchin (Pseudocentrotus depressus)
C:Species: Pseudocentrotus depressus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Aug-2000
C:Accession: E60788
R:Suzuki, N.; Kajitara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentro
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: E60788
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction.
C:Superfamily: unassigned animal peptides

Query Match 34.0%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGG 7
|:|
Db 2 FDLGG 7

Search completed: August 30, 2004, 10:58:47
Job time : 3.70608 secs


```
FILE REFERENCE: 3190-049
CURRENT APPLICATION NUMBER: US/10/788,016
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: PCT/JP02/08641
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: JP P2001-260046
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Peptide consisting of 9 amino acid residues from the 91st residue
OTHER INFORMATION: to the 99th residue of cyclophilin B
US-10-788-016-2

Query Match
Best Local Similarity 100.0%; Score 50; DB 16; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
DB 1 DFMIOGGDF 9

RESULT 3
US-10-788-016-9
Sequence 9, Application US/10788016
Publication No. US2004014192A1
GENERAL INFORMATION:
APPLICANT: ITOH, Kyogo
TITLE OF INVENTION: Desensitizers
FILE REFERENCE: 3190-049
CURRENT APPLICATION NUMBER: US/10/788,016
CURRENT FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: PCT/JP02/08641
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: JP P2001-260046
PRIOR FILING DATE: 2001-08-29
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 9
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Designed peptide based on the peptide consisting of 9 amino acid
OTHER INFORMATION: residues from the 91st residue to the 99th residue of
US-10-788-016-9

Query Match
Best Local Similarity 94.0%; Score 47; DB 16; Length 9;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DFMIOGGDF 9
DB 1 DFMIOGGDF 9

RESULT 4
US-10-014-340-347
Sequence 347, Application US/10014340
Publication No. US2003006441A1
GENERAL INFORMATION:
APPLICANT: Herath, et al
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
FILE REFERENCE: 9195-078
CURRENT APPLICATION NUMBER: US/10/014,340
CURRENT FILING DATE: 2001-12-10
```

```
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.0
SEQ ID NO 347
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-340-347

Query Match
Best Local Similarity 78.0%; Score 39; DB 12; Length 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMCQGGDF 9
DB 5 FMCQGGDF 12

RESULT 5
US-09-846-350-1
Sequence 1, Application US/09846350
Patent No. US20020161188A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having a Molecular
FILE REFERENCE: 2132.025
CURRENT APPLICATION NUMBER: US/09/846,350
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-846-350-1

Query Match
Best Local Similarity 54.0%; Score 27; DB 9; Length 10;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
DB 1 DFLAEGG 7

RESULT 6
US-09-846-342-1
Sequence 1, Application US/09846342
Patent No. US20020160422A1
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
FILE REFERENCE: 2132.026
CURRENT APPLICATION NUMBER: US/09/846,342
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-846-342-1

Query Match
Best Local Similarity 54.0%; Score 27; DB 9; Length 11;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
DB 2 DFLAEGG 8
```

```
RESULT 7
US-10-356-257-161
; Sequence 161, Application US/10356257
; Publication No. US2004008767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUD, HENRY R.
; TITLE OF INVENTION: FV1A Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 161
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: sequence is synthesized
US-10-356-257-161

Query Match
Best Local Similarity 54.0%; Score 27; DB 16; Length 11;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 FMIOGG 7
Db 6 FMVREG 11

RESULT 8
US-09-845-725-1
; Sequence 1, Application US/09845725
; Patent No. US2002016185A1
; GENERAL INFORMATION:
; APPLICANT: JACKOWSKI, GEORGE
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.028
; CURRENT APPLICATION NUMBER: US/09/845,725
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-725-1

Query Match
Best Local Similarity 54.0%; Score 27; DB 9; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFMIQGG 7
Db 3 DFVREG 9

RESULT 9
US-09-845-729-1
; Sequence 1, Application US/09845729
; Publication No. US20020160528A1
; GENERAL INFORMATION:
; APPLICANT: JACKOWSKI, GEORGE
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.031
; CURRENT APPLICATION NUMBER: US/09/845,729
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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```
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-729-1

Query Match
Best Local Similarity 54.0%; Score 27; DB 12; Length 13;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DFMIQGG 7
Db 4 DFVREG 10

RESULT 10
US-10-363-791-103
; Sequence 103, Application US/10363791
; Publication No. US20040029197A1
; GENERAL INFORMATION:
; APPLICANT: TAKIMOTO, Masato
; APPLICANT: KUZUMAKI, No. US20040029197A1oru
; APPLICANT: SATO, No. US20040029197A1ilyuki
; TITLE OF INVENTION: A novel human cancer/testis-associated gene theroef
; FILE REFERENCE: 4439-4006
; CURRENT APPLICATION NUMBER: US/10/363,791
; CURRENT FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: JP 2000-274218
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-791-103

Query Match
Best Local Similarity 52.0%; Score 26; DB 12; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DFMIQGGDF 9
Db 1 DFVREGDF 9

RESULT 11
US-09-988-493-263
; Sequence 263, Application US/09988493
; Publication No. US20030064419A1
; GENERAL INFORMATION:
; APPLICANT: Herath, Herath Modiyanselage Athula Chandrasiri
; APPLICANT: O'Hare, Michael John
; APPLICANT: Page, Martin John
; APPLICANT: Parekh, Rajesh Bhikhu
; TITLE OF INVENTION: Waterfield, Michael Derek
; TITLE OF INVENTION: Proteins, Genes, and Their Use for
; FILE REFERENCE: 2543-1-024
; CURRENT APPLICATION NUMBER: US/09/988,493
; CURRENT FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: PCT/GB01/01219
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: GB 0006695.1
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: GB 0007265.2
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapien
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US-09-988-493-263

Query Match
Best Local Similarity 52.0%; Score 26; DB 12; Length 14;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DMIQGGDF 9
DB 1 DSLLDGDF 9

RESULT 12
US-10-285-394-75
; Sequence 75, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: PASILLO, LISA M.
; APPLICANT: HERATH, HERATH MUDIYANSILAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003.01
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-75

Query Match
Best Local Similarity 52.0%; Score 26; DB 15; Length 14;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DMIQGGDF 9
DB 1 DSLLDGDF 9

RESULT 13
US-10-182-252A-872
; Sequence 872, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUDS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 872
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-872

Query Match
Best Local Similarity 50.0%; Score 25; DB 12; Length 9;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIQGGDF 9
DB 1 MIQGNF 7

RESULT 14
US-10-057-475B-10856
; Sequence 10856, Application US/10057475B
; Publication No. US2004002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordenez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-01440205
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10856
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Ly1484 long MHC HLA A2 class I binding peptide
US-10-057-475B-10856

Query Match
Best Local Similarity 50.0%; Score 25; DB 15; Length 9;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 IQGGDF 9
DB 2 LOGGSF 7

RESULT 15
US-10-057-475B-10911


```

; Sequence 10911, Application US/10057475B
; Publication No. US20040002068A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Clapper, Jonathan David
; APPLICANT: Wang, Aijun
; APPLICANT: Ordóñez, Nadia
; APPLICANT: Carter, Lauren
; APPLICANT: McNeill, Patricia Dianne
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-014402US
; CURRENT APPLICATION NUMBER: US/10/057,475B
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10979
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10911
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 short MHC HLA A2 class I binding peptide
US-10-057-475B-10911

Query Match          50.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 4 IGGDF 9
   :|||
Db 2 LGGGSF 7

RESULT 16
US-10-154-884B-10856
; Sequence 10856, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126

```

```

; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10856
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Ly1484 long MHC HLA A2 class I binding peptide
US-10-154-884B-10856

Query Match          50.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 4 IGGDF 9
   :|||
Db 2 LGGGSF 7

RESULT 17
US-10-154-884B-10911
; Sequence 10911, Application US/10154884B
; Publication No. US20040005561A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Retter, Marc W.
; APPLICANT: Corixa Corporation
; TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
; FILE REFERENCE: 014058-013521US
; CURRENT APPLICATION NUMBER: US/10/154,884B
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: US 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: US 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: US 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: US 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 60/222,903

```

```
; PRIOR FILING DATE: 2000-08-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 11290
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10911
; LENGTH: 9
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Lyl484 short MHC HLA A2 class I binding peptide
US-10-154-884B-10911

Query Match
Best Local Similarity 50.0%; Score 25; DB 15; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 ICGDF 9
Db 2 LOGGSF 7

RESULT 18
US-09-966-871-26
; Sequence 26, Application US/09966871
; Patent No. US20020127539A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; TITLE OF INVENTION: Assays for Identifying Receptors Having
; FILE REFERENCE: 00398/512002
; CURRENT APPLICATION NUMBER: US/09/966,871
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/236,302
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/289,644
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-966-871-26

Query Match
Best Local Similarity 48.0%; Score 24; DB 9; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOGG 7
Db 1 FMVLGG 6

RESULT 19
US-10-458-860-26
; Sequence 26, Application US/10458860
; Publication No. US20040049800A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Rapid Methods For Assessing Therapeutic
; TITLE OF INVENTION: Activity Using Animals Expressing Constitutively Active G
; FILE REFERENCE: 00398/517002
; CURRENT APPLICATION NUMBER: US/10/458,860
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: US 60/388,450
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRF
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic fragment
US-10-458-860-26

Query Match
Best Local Similarity 48.0%; Score 24; DB 12; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOGG 7
Db 1 FMVLGG 6

RESULT 20
US-10-039-645-26
; Sequence 26, Application US/10039645
; Publication No. US20020147170A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Constitutively Active, Hypersensitive,
; FILE REFERENCE: 00398/510002
; CURRENT APPLICATION NUMBER: US/10/039,645
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: US 60/243,550
; PRIOR FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-039-645-26

Query Match
Best Local Similarity 48.0%; Score 24; DB 13; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOGG 7
Db 1 FMVLGG 6

RESULT 21
US-10-139-084-26
; Sequence 26, Application US/10139084
; Publication No. US20030087313A1
; GENERAL INFORMATION:
; APPLICANT: Kopin, Alan S.
; APPLICANT: Beinborn, Martin
; TITLE OF INVENTION: Dose Response-Based Methods For
; FILE REFERENCE: 00398/515002
; CURRENT APPLICATION NUMBER: US/10/139,084
; PRIOR FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/288,647
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 12
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-139-084-26

Query Match
Best Local Similarity 48.0%; Score 24; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOGG 7
Db 1 FMVLGG 7
```

Db 1 FMTLOG 6

RESULT 22
US-10-469-304-122
; Sequence 122, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 122
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-122

Query Match
Best Local Similarity 48.0%; Score 24; DB 16; Length 13;
Best Local Similarity 57.1%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDP 9
:|||||:
7 LIQNGDW 13

RESULT 23
US-10-469-304-123
; Sequence 123, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 123
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-123

Query Match
Best Local Similarity 48.0%; Score 24; DB 16; Length 13;
Best Local Similarity 57.1%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDP 9
:|||||:
5 LIQNGDW 11

RESULT 24
US-10-469-304-124
; Sequence 124, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT

US-10-469-304-125
; Sequence 125, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-125

Query Match
Best Local Similarity 48.0%; Score 24; DB 16; Length 13;
Best Local Similarity 57.1%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDP 9
:|||||:
1 LIQNGDW 7

RESULT 25
US-10-469-304-125
; Sequence 125, Application US/10469304
; Publication No. US20040091974A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; TITLE OF INVENTION: Anti HLA-DR antibody
; FILE REFERENCE: PH-1646-PCT
; CURRENT APPLICATION NUMBER: US/10/469,304
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: JP2001/317054
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 125
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-125

Query Match
Best Local Similarity 48.0%; Score 24; DB 16; Length 13;
Best Local Similarity 57.1%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDP 9
:|||||:
1 LIQNGDW 7

RESULT 26
US-10-285-394-239
; Sequence 239, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: FASULO, LISA M.
; APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003.01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/335,964
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 239

```
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-239
```

```
Query Match          48.0%; Score 24; DB 15; Length 14;
Best Local Similarity 42.9%; Pred. No. 9.8e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 MIOGGDF 9
    |||
Db 1 LIEAGDF 7
```

```
RESULT 27
US-10-467-113-6
; Sequence 6, Application US/10467113
; Publication No. US20040063634A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED KERATINOCYTE GROWTH FACTOR
; FILE REFERENCE: MER-111
; CURRENT APPLICATION NUMBER: US/10/467,113
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102574.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01175
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-467-113-6
```

```
Query Match          47.0%; Score 23.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 DFMIOGCD 8
    |||
Db 4 DYM-EGGD 10
```

```
RESULT 28
US-10-467-113-7
; Sequence 7, Application US/10467113
; Publication No. US20040063634A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED KERATINOCYTE GROWTH FACTOR
; FILE REFERENCE: MER-111
; CURRENT APPLICATION NUMBER: US/10/467,113
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102574.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01175
; PRIOR FILING DATE: 2002-02-05
```

```
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-467-113-7
```

```
Query Match          47.0%; Score 23.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 DFMIOGCD 8
    |||
Db 2 DYM-EGGD 8
```

```
RESULT 29
US-10-467-113-8
; Sequence 8, Application US/10467113
; Publication No. US20040063634A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; TITLE OF INVENTION: MODIFIED KERATINOCYTE GROWTH FACTOR
; FILE REFERENCE: MER-111
; CURRENT APPLICATION NUMBER: US/10/467,113
; PRIOR FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102574.0
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01175
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-467-113-8
```

```
Query Match          47.0%; Score 23.5; DB 12; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
```

```
QY 1 DFMIOGCD 8
    |||
Db 1 DYM-EGGD 7
```

```
RESULT 30
US-10-468-370-267
; Sequence 267, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
```

```

; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 267
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-267

```

```

Query Match          47.0%; Score 23.5; DB 16; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 1 DEMIOGGD 8
    | : | | |
Db 4 DYM-EGGD 10

```

```

RESULT 31
; Sequence 268, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 268
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-268

```

```

Query Match          47.0%; Score 23.5; DB 16; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 1 DEMIOGGD 8
    | : | | |
Db 2 DYM-EGGD 8

```

```

RESULT 32
; Sequence 269, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-118
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-269

```

```

Query Match          47.0%; Score 23.5; DB 16; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```

```

QY 1 DEMIOGGD 8
    | : | | |
Db 1 DYM-EGGD 7

```

```

RESULT 33
; Sequence 31, Application US/10359363A
; Publication No. US20030228371A1
; GENERAL INFORMATION:
; APPLICANT: Skinner, James E.
; APPLICANT: Anchin, Jerry M.
; TITLE OF INVENTION: ANTI-INFARCTION MOLECULES
; FILE REFERENCE: 22118.0001U4
; CURRENT APPLICATION NUMBER: US/10/359,363A
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/429,278
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/392,133
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/354,678
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030228371A1e =
; OTHER INFORMATION: Synthetic Construct

```

US-10-359-363A-31

Query Match 46.0%; Score 23; DB 15; Length 8;
Best Local Similarity 42.9%; Pred. No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
: : : :
Db 2 EFLABCG 8

RESULT 34

US-10-601-837-86
; Sequence 86, Application US/10601837
; Publication No. US20040053309A1
; GENERAL INFORMATION:
; APPLICANT: Holt, Gordon D
; APPLICANT: Kelly, Michael D
; APPLICANT: Kennedy, Sandra J
; APPLICANT: Moyes, Christopher
; TITLE OF INVENTION: Proteins, Genes and Their Use for Diagnosis and Treatment of Kidney
; FILE REFERENCE: 2543-1-030
; CURRENT APPLICATION NUMBER: US/10/601,837
; CURRENT FILING DATE: 2003-06-23
; PRIOR APPLICATION NUMBER: PCT/GB01/05777
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: US 60/260392
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Rattus No. US20040053309A1vegicus
US-10-601-837-86

Query Match 46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
: : : :
Db 2 DFCIOVG 8

RESULT 35

US-10-014-340-253
; Sequence 253, Application US/10014340
; Publication No. US20030064411A1
; GENERAL INFORMATION:
; APPLICANT: Herath, et al
; TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
; FILE REFERENCE: 9195-078
; CURRENT APPLICATION NUMBER: US/10/014,340
; CURRENT FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 253
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-014-340-253

Query Match 46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
: : : :
Db 2 DFCIOVG 8

RESULT 36

US-10-182-252A-281
; Sequence 281, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 281
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-182-252A-281

Query Match 46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDP 9
: : : :
Db 1 MIOGDP 7

RESULT 37

US-10-182-252A-282
; Sequence 282, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUS, SOREN
; APPLICANT: CORBET, SYLVIE
; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 282
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-182-252A-282

Query Match 46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDF 9
Db 1 MLQGNF 7

RESULT 38
US-10-182-252A-878
Sequence 878, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 878
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-878

Query Match 46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDF 9
Db 1 MLQGNF 7

RESULT 39
US-10-182-252A-879
Sequence 879, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 879
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-879

Query Match 46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDF 9
Db 1 MLQGNF 7

RESULT 40
US-10-182-252A-880
Sequence 880, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 880
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-880

Query Match 46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDF 9
Db 1 MLQGNF 7

RESULT 41
US-10-182-252A-881
Sequence 881, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS

```
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 881
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-881
```

```
Query Match          46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 MIOGDF 9
       1 MLORGNF 7
Db
```

```
RESULT 42
US-10-182-252A-882
Sequence 882, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUTS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 882
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-882
```

```
Query Match          46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 MIOGDF 9
       1 MLORGNF 7
Db
```

```
RESULT 43
US-10-182-252A-883
Sequence 883, Application US/10182252A
Publication No. US20040072162A1
```

```
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUTS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 883
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-883
```

```
Query Match          46.0%; Score 23; DB 12; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 MIOGDF 9
       1 MLORGNF 7
Db
```

```
RESULT 44
US-10-283-741-30
Sequence 30, Application US/10283741
Publication No. US20030182068A1
GENERAL INFORMATION:
APPLICANT: Battersby, Bronwyn J.
APPLICANT: Miller, Christopher R.
APPLICANT: Trau, Mathias
APPLICANT: May, Jeffrey C.
APPLICANT: Johnston, Angus
TITLE OF INVENTION: Device and Methods For Directed
FILE REFERENCE: 50277/003002
CURRENT APPLICATION NUMBER: US/10/283,741
CURRENT FILING DATE: 2002-10-30
PRIOR APPLICATION NUMBER: US 60/330,759
PRIOR FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 30
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-283-741-30
```

```
Query Match          46.0%; Score 23; DB 14; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DFMIOS 6
       4 EFMIDG 9
Db
```


Thu Sep 2 07:41:31 2004

us-09-720-469a-2.aug30.rapb

Page 13

```
RESULT 45
US-10-359-363A-30
; Sequence 30, Application US/10359363A
; Publication No. US20030228371A1
; GENERAL INFORMATION:
; APPLICANT: Skinner, James E.
; APPLICANT: Auchin, Jerry M.
; TITLE OF INVENTION: ANTI-INFACTION MOLECULES
; FILE REFERENCE: 22118.0001U4
; CURRENT APPLICATION NUMBER: US/10/359,363A
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: 60/429,278
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: 60/392,133
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: 60/354,678
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 9
; TYPE: PR
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/No. US20030228371A1e =
US-10-359-363A-30

Query Match          46.0% Score 23; DB 15; Length 9;
Best Local Similarity 42.9%; Pred No. 1.2e+06;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DFMIOGG 7
       :|:|:|
Db      2 EPLAEGG 8
```

Search completed: August 30, 2004, 11:04:53
Job time : 13.0068 secs

Thu Sep 2 07:41:31 2004

us-09-720-469a-2.aug30.ra1

Page 1

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:59 ; Search time 3.55743 Seconds
(without alignments)
130.609 Million cell updates/sec

Title: US-09-720-469A-2
Perfect score: 50
Sequence: 1 DFMIGGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 78885

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	56.0	12	2	US-08-406-330-75 Sequence 75, Appl
2	28	56.0	12	2	US-08-556-597-75 Sequence 75, Appl
3	27	54.0	10	6	5196404-18 Patent No. 5196404
4	27	54.0	10	6	5433940-25 Patent No. 5433940
5	27	54.0	12	4	US-09-846-350A-1 Sequence 1, Appl
6	27	54.0	14	4	US-09-845-725A-1 Sequence 1, Appl
7	25	50.0	9	1	US-08-457-172-1 Sequence 1, Appl
8	24	48.0	8	2	US-08-459-568-75 Sequence 75, Appl
9	24	48.0	8	2	US-08-399-411-75 Sequence 75, Appl
10	24	48.0	8	3	US-08-516-859A-75 Sequence 75, Appl
11	24	48.0	8	4	US-09-586-472-75 Sequence 75, Appl
12	24	48.0	8	4	US-09-528-706-75 Sequence 75, Appl
13	24	48.0	10	4	US-08-765-953-8 Sequence 62, Appl
14	24	48.0	8	1	US-08-487-860-62 Sequence 48, Appl
15	23	46.0	9	1	US-08-704-170-48 Sequence 48, Appl
16	23	46.0	9	5	PCT-US94-02631-48 Sequence 5, Appl
17	23	46.0	14	1	US-08-513-841-5 Sequence 6, Appl
18	23	46.0	14	2	US-08-696-834-6 Sequence 5, Appl
19	23	46.0	14	2	US-08-942-673-5 Sequence 14, Appl
20	23	46.0	14	3	US-09-158-427-14 Sequence 5, Appl
21	23	46.0	14	3	US-09-118-317-5 Sequence 7, Appl
22	22	44.0	9	1	US-08-215-805A-7 Sequence 52, Appl
23	22	44.0	9	1	US-08-215-805A-52 Sequence 21, Appl
24	22	44.0	10	1	US-08-215-805A-58 Sequence 23, Appl
25	22	44.0	10	3	US-08-658-130-21 Sequence 21, Appl
26	22	44.0	10	3	US-08-981-122-23 Sequence 21, Appl
27	22	44.0	10	5	PCT-US96-08723-21 Sequence 21, Appl

28	22	44.0	11	4	US-09-026-276-23 Sequence 23, Appl
29	22	44.0	11	4	US-09-964-201A-23 Sequence 23, Appl
30	22	44.0	12	1	US-08-082-849B-15 Sequence 15, Appl
31	22	44.0	12	4	US-09-785-921A-13 Sequence 13, Appl
32	22	44.0	12	5	PCT-US94-0162A-15 Sequence 15, Appl
33	22	44.0	13	1	US-07-847-743B-5 Sequence 5, Appl
34	22	44.0	13	1	US-08-036-555B-31 Sequence 31, Appl
35	22	44.0	13	1	US-08-469-569-31 Sequence 31, Appl
36	22	44.0	13	1	US-08-456-201-5 Sequence 5, Appl
37	22	44.0	13	1	US-08-249-322A-13 Sequence 31, Appl
38	22	44.0	13	1	US-08-469-526A-31 Sequence 5, Appl
39	22	44.0	13	2	US-08-330-161-5 Sequence 5, Appl
40	22	44.0	13	2	US-08-456-241-5 Sequence 31, Appl
41	22	44.0	13	2	US-08-734-591A-31 Sequence 31, Appl
42	22	44.0	13	2	US-08-440-401-5 Sequence 5, Appl
43	22	44.0	13	2	US-08-419-878B-5 Sequence 5, Appl
44	22	44.0	13	2	US-08-469-660-31 Sequence 31, Appl
45	22	44.0	13	3	US-08-470-335-31 Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-08-406-330-75
Sequence 75, Application US/08406330
Patent No. 5817748
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN IB/IX
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESSES:
ADDRESS: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-75
Query Match 56.0% Score 28; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

RESULT 2

US-08-556-597-75
Sequence 75, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: MINOTOPES AND ANTI-MINOTOPES OF
TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-75

Query Match 56.0%; Score 28; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 50;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 FMIQGG 9
DB 1 FVVRGGTF 8

RESULT 3

5196404-18
Patent No. 5196404
APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
TITLE OF INVENTION: INHIBITORS OF THROMBIN
NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/549,388
FILING DATE: 06-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 395,482
FILING DATE: 18-AUG-1989
SEQ ID NO:18
LENGTH: 10
5196404-18

Query Match 54.0%; Score 27; DB 6; Length 10;
Best Local Similarity 57.1%; Pred. No. 61;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFMIQGG 7
DB 2 DFLAEGG 8

RESULT 4

5433940-25
Patent No. 5433940
APPLICANT: MARAGANORE, JOHN M.; FENTON II, JOHN M.; KLINE, TONI
TITLE OF INVENTION: INHIBITORS OF THROMBIN
NUMBER OF SEQUENCES: 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,259
FILING DATE: 17-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 548,388
FILING DATE: 06-JUL-1989
APPLICATION NUMBER: 395,482
FILING DATE: 18-AUG-1989
SEQ ID NO:25
LENGTH: 10
5433940-25

Query Match 54.0%; Score 27; DB 6; Length 10;
Best Local Similarity 57.1%; Pred. No. 61;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFMIQGG 7
DB 2 DFLAEGG 8

RESULT 5

US-09-846-350A-1
Sequence 1, Application US/09846350A
Patent No. 6599877
GENERAL INFORMATION:
APPLICANT: Jackowski, George
APPLICANT: Marshall, John
APPLICANT: Vreese, Tammy
APPLICANT: Thatcher, Brad
TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having A Molecular
FILE REFERENCE: 2132.025
CURRENT APPLICATION NUMBER: US/09/846,350A
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-846-350A-1

Query Match 54.0%; Score 27; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 75;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DFMIQGG 7
DB 2 DFLAEGG 8

RESULT 6

US-09-845-725A-1
Sequence 1, Application US/09845725A
Patent No. 6627608
GENERAL INFORMATION:
APPLICANT: Jackowski, George
TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
TITLE OF INVENTION: OF 1206 DALTONS

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Page 3

FILE REFERENCE: 2132.028
CURRENT APPLICATION NUMBER: US/09/845,725A
CURRENT FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patent in version 3.1
SEQ ID NO: 1
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-845-725A-1

Query Match 54.0%; Score 27; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPMIOGG 7
Db 4 DFLAEGG 10

RESULT 7
US-08-457-172-1
Sequence 1, Application US/08457172
Patent No. 5622837
GENERAL INFORMATION:
APPLICANT: Hans Scheefers, Ursula Scheefers-Borchel and
APPLICANT: Andreas Szisgoleit
TITLE OF INVENTION: PANCREAS ELASTASE 1-SPECIFIC ANTIBODY, A PROCESS FOR
TITLE OF INVENTION: OBTAINING IT, AND A TEST KIT CONTAINING SUCH ANTIBODY
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,172
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/220,395
FILING DATE:
APPLICATION NUMBER: US 07/969,173
FILING DATE: 29-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42883/JPM/ATM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 977-9809
TELEX: 422523 COOP UI
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
CELL TYPE: pancreatic
US-08-457-172-1

Query Match 50.0%; Score 25; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 3e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 3 MIOGGD 8
Db 2 MVAGGD 7

RESULT 8
US-08-459-568-75
Sequence 75, Application US/08459568
Patent No. 5811304
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,568
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-459-568-75

Query Match 48.0%; Score 24; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MIOGGD 8
Db 3 LVBGGD 8

RESULT 9
US-08-399-411-75
Sequence 75, Application US/08399411
Patent No. 5831008
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
TITLE OF INVENTION: Zinc Finger Proteins
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA

ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,411
FILING DATE: 06-MAR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-399-411-75

Query Match 48.0%; Score 24; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOGSD 8
DB 3 LIEGSD 8

RESULT 10
US-08-516-859A-75
Sequence 75, Application US/08516859A
Patent No. 6069231
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSES:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/516,859A
FILING DATE: 18-AUG-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-516-859A-75

Query Match 48.0%; Score 24; DB 3; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOGSD 8
DB 3 LIEGSD 8

RESULT 11
US-09-586-472-75
Sequence 75, Application US/09586472
Patent No. 632335
GENERAL INFORMATION:
APPLICANT: Huang, Shi
TITLE OF INVENTION: Retinoblastoma Protein - Interacting
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSES:
ADDRESSER: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/586,472
FILING DATE: 01-Jun-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/528,706
FILING DATE: 17-MAR-2000
APPLICATION NUMBER: US 08/516,859
FILING DATE: 18-AUG-1995
APPLICATION NUMBER: US 08/399,411
FILING DATE: 06-MAR-1995
APPLICATION NUMBER: US 08/292,683
FILING DATE: 18-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 4130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-586-472-75

Query Match 48.0%; Score 24; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOGSD 8
DB 3 LIEGSD 8

RESULT 12

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US-09-528-706-75

Sequence 75, Application US/09528706
Patent No. 6468985

GENERAL INFORMATION:

APPLICANT: Huang, Shi

TITLE OF INVENTION: Retinoblastoma Protein - Interacting

TITLE OF INVENTION: Zinc Finger Proteins

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/528,706

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/516,859

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/292,683

FILING DATE: 18-AUG-1994

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 1776

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 75:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-09-528-706-75

Query Match 48.0%; Score 24; DB 4; Length 8;

Best Local Similarity 50.0%; Pred. No. 3e+05;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOGCD 8

DB 3 LIEGCD 8

RESULT 13

US-08-765-953-8

Sequence 8, Application US/08765953

Patent No. 6342201

GENERAL INFORMATION:

APPLICANT: DINKELBORG, LUDGER

APPLICANT: STEPHAN, CHRISTOPH

APPLICANT: SEMMLER, WOLFHARD

APPLICANT: SPECK, ULRICH

APPLICANT: KENKLEIN, PETER

TITLE OF INVENTION: COMPLEX COMPOUNDS FOR DIAGNOSIS OF

TITLE OF INVENTION: VASCULAR DISEASES

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: WOOD, PHILLIPS, VAN SANTEN, CLARK & MORTIMER

QY 6 GGDF 9

DB 1 GGDF 4

RESULT 14

US-08-487-860-62

Sequence 62, Application US/08487860

Patent No. 5792456

GENERAL INFORMATION:

APPLICANT: Yelton, Dale

APPLICANT: Glaser, Scott

APPLICANT: Huse, William

APPLICANT: Rosok, Mae J.

TITLE OF INVENTION: No. 5792456e1 Mutant BR96 Antibodies and

TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

QY 6 GGDF 9

DB 1 GGDF 4

RESULT 14

US-08-487-860-62

Sequence 62, Application US/08487860

Patent No. 5792456

GENERAL INFORMATION:

APPLICANT: Yelton, Dale

APPLICANT: Glaser, Scott

APPLICANT: Huse, William

APPLICANT: Rosok, Mae J.

TITLE OF INVENTION: No. 5792456e1 Mutant BR96 Antibodies and

TITLE OF INVENTION: Functional Equivalents Reactive With Human Carcinomas

NUMBER OF SEQUENCES: 62

CORRESPONDENCE ADDRESS:

ADDRESSEE: Merchant & Gould

Page 5

REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436.16US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-487-860-62

Query Match 46.0%; Score 23; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCGD 8
DB 2 QCGD 5

RESULT 15
US-08-704-170-48
Sequence 48, Application US/08704170
Patent No. 5707626
GENERAL INFORMATION:
APPLICANT: Douvas, Angelina
APPLICANT: Takehana, Yoshi
APPLICANT: Ehresmann, Glenn
TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESSES:
ADDRESSER: Robbins, Berline & Carson
STREET: 201 No. 5707626th Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,170
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,850
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1920-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-704-170-48

Query Match 46.0%; Score 23; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFMIOGSD 8

DB 1 EFLRGGSD 8

RESULT 16
PCT-US94-02631-48
Sequence 48, Application PC/TUS9402631
GENERAL INFORMATION:
APPLICANT: Douvas, Angelina
APPLICANT: Takehana, Yoshi
APPLICANT: Ehresmann, Glenn
TITLE OF INVENTION: THERAPEUTIC STRATEGIES FOR
IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
TITLE OF INVENTION: IMMUNOINFECTION CLUSTER VIRUS INFECTIONS
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESSES:
ADDRESSER: Robbins, Berline & Carson
STREET: 201 North Figueroa Street, Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02631
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/029,850
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1920-331
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-02631-48

Query Match 46.0%; Score 23; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFMIOGSD 8
DB 1 EFLRGGSD 8

RESULT 17
US-08-513-841-5
Sequence 5, Application US/08513841
Patent No. 5753481
GENERAL INFORMATION:
APPLICANT: Niwa, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshinori
APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiroshi
TITLE OF INVENTION: No. 5753481 L-sorbose Dehydrogenase and No. 5753481 L-sorbose
Dehydrogenase Obtained from Gluconobacter oxydans T-100
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSER: Obion, McTearland, Walter & Neustradt, P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400

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Page 7

CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,841
FILING DATE: 01-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 9304700.9
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-909-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-841-5

Query Match 46.0%; Score 23; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 4.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
Db 5 DYIVGG 11

RESULT 18
US-08-696-834-6
Sequence 6, Application US/08696834
Patent No. 5834263
GENERAL INFORMATION:
APPLICANT: Niwa, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshihori
APPLICANT: Yoshida, Masaru
APPLICANT: Hayashi, Hiromi
TITLE OF INVENTION: Method for Producing 2-Keto-L-Gulonic Acid
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,834
FILING DATE: 24-SEP-1996
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 28612/1994
FILING DATE: 25-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-834-6

Query Match 46.0%; Score 23; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 4.5e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
Db 5 DYIVGG 11

RESULT 19
US-08-942-673-5
Sequence 5, Application US/08942673
Patent No. 5861292
GENERAL INFORMATION:
APPLICANT: Niwa, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshihori
APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiromi
TITLE OF INVENTION: No. 5861292e1 L-sorbose Dehydrogenase and No. 5861292e1
TITLE OF INVENTION: L-sorbose Dehydrogenase Obtained from Gluconobacter
TITLE OF INVENTION: oxydans T-100
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oblon, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/942,673
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,841
FILING DATE: 01-NOV-1995
APPLICATION NUMBER: UK 9304700.9
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-909-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220

TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-942-673-5

Query Match
Best Local Similarity 46.0%; Score 23; DB 2; Length 14;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPMIOGG 7
Db 5 DVIWVG 11

RESULT 20
US-09-155-427-14
Sequence 14, Application US/09155427A
Patent No. 6159704
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A
TITLE OF INVENTION: Phosphatase Modulator
FILE REFERENCE: 4-20803/A/PCT
CURRENT APPLICATION NUMBER: US/09/155,427A
CURRENT FILING DATE: 1998-09-28
EARLIER APPLICATION NUMBER: PCT/EP97/01330
EARLIER FILING DATE: 1997-03-17
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 14
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide
US-09-155-427-14

Query Match
Best Local Similarity 46.0%; Score 23; DB 3; Length 14;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 OGGD 8
Db 2 OGGD 5

RESULT 21
US-09-118-317-5
Sequence 5, Application US/09118317
Patent No. 6197562
GENERAL INFORMATION:
APPLICANT: Niwa, Mineo
APPLICANT: Saito, Yoshimasa
APPLICANT: Ishii, Yoshinori
APPLICANT: Yoshida, Masaru
APPLICANT: Suzuki, Hiroki
TITLE OF INVENTION: No. 6197562el L-sorbose Dehydrogenase and No. 6197562el
TITLE OF INVENTION: L-sorbose Dehydrogenase Obtained from Gluconobacter
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ojion, Spivak, McClelland, Maier & Neustadt, P.C.
STREET: 1755 Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS-DOS Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/118,317
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/513,841
FILING DATE: 01-NOV-1995
APPLICATION NUMBER: UK 9304700.9
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA: JP 241851/1993
APPLICATION NUMBER: JP 241851/1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 18-909-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-118-317-5

Query Match
Best Local Similarity 46.0%; Score 23; DB 3; Length 14;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPMIOGG 7
Db 5 DVIWVG 11

RESULT 22
US-08-215-805A-7
Sequence 7, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA
TITLE OF INVENTION: SUI5
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Pasteurella suis
STRAIN: 5943
IMMEDIATE SOURCE:
LIBRARY: P. suis DNA in Bacteriophage lambda-dash
CLONE: (lambda)yfc33-37
US-08-215-805A-7

Query Match 44.0%; Score 22; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IQGSD 8
: : : : :
Db 1 IEGSD 5

RESULT 23
US-08-215-805A-52
Sequence 52, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA
TITLE OF INVENTION: SUIIS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
US-08-215-805A-52

Query Match 44.0%; Score 22; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 IQGSD 8
: : : : :
Db 1 IEGSD 5

RESULT 24
US-08-215-805A-58
Sequence 58, Application US/08215805A
Patent No. 5559008
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
TITLE OF INVENTION: LEUKOTOXIN GENE FROM PASTURELLA
TITLE OF INVENTION: SUIIS
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/215,805A
FILING DATE: 22-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19603/61 (D-1329A)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Actinobacillus pleuropneumoniae
US-08-215-805A-58

Query Match 44.0%; Score 22; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 3e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 IQGSD 8
: : : : :
Db 1 IEGSD 5

RESULT 25
US-08-658-130-21
Sequence 21, Application US/08658130
Patent No. 5736392
GENERAL INFORMATION:
APPLICANT: Hawley-Nelson, Pamela
APPLICANT: Lan, Jiangling
APPLICANT: Shih, Polen
APPLICANT: Jesse, Joel A.
APPLICANT: Shifferli, Kevin P.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLE OF INVENTION: Transfections
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,130
FILING DATE: 04-JUN-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/477,354
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 32-95A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ. ID NO.: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
US-08-658-130-21

Query Match
Best Local Similarity 44.0%; Score 22; DB 1; Length 10;
Pred. No. 4,7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGGDF 9
DB 3 IRGGTF 8

RESULT 26
US-08-981-122-23
Sequence 23, Application US/08981122B
GENERAL INFORMATION:
APPLICANT: Hatanaka, Yoshihiro
APPLICANT: Aricomi, Masaharu
TITLE OF INVENTION: peptide for binding thereto a low density lipoprotein
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/981,122B
PRIORITY FILING DATE: 1997-12-18
PRIOR APPLICATION NUMBER: JP 7-176904
PRIOR FILING DATE: 1995-06-21
PRIOR APPLICATION NUMBER: PCT/JP96/01734
PRIOR FILING DATE: 1996-06-21
NUMBER OF SEQ. ID NOS: 90
SOFTWARE: PatentIn Ver. 2.0
SEQ. ID NO. 23
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence of a peptide synthesized in Example 3 from L-form
PATENT NO. 6127339
OTHER INFORMATION: Fmoc amino acids by solid phase method using a multipetide
US-08-981-122-23

Query Match
Best Local Similarity 44.0%; Score 22; DB 3; Length 10;
Pred. No. 4,7e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 FMIOGG 7
DB 1:::111
```

```
DB 2 FLMRGG 7

RESULT 27
PCT-US96-08723-21
Sequence 21, Application PC/TUS9608723
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
TITLE OF INVENTION: Peptide-Enhanced Cationic Lipid
TITLE OF INVENTION: Transfections
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08723
FILING DATE: 04-JUN-1996
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/477,354
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 3295A WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080\
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ. ID NO.: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: protein
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
PCT-US96-08723-21

Query Match
Best Local Similarity 44.0%; Score 22; DB 5; Length 10;
Pred. No. 4,7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 IGGDF 9
DB 3 IRGGTF 8

RESULT 28
US-09-026-276-23
Sequence 23, Application US/09026276
GENERAL INFORMATION:
PATENT NO. 6319503
APPLICANT: Kenten, John H.
APPLICANT: Tramotoano, Alfonso
APPLICANT: Pilon, April L.
APPLICANT: Lobas, Gerald L.
APPLICANT: Roberts, Steven F.
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6319503 09/026,276
CURRENT APPLICATION NUMBER: US/09/026,276
CURRENT FILING DATE: 1998-02-19
NUMBER OF SEQ. ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
```

SEQ ID NO 23
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-026-276-23

Query Match 44.0%; Score 22; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCGDF 9
Db 1 RCGDY 5

RESULT 29
US-09-964-201A-23
Sequence 23, Application US/09964201A
Patent No. 6660271
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Tramotoano, Alfonso
APPLICANT: Pilon, Aprille L
APPLICANT: Lohnas, Gerald L
APPLICANT: Roberts, Steven F
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6660271 09/026,276
CURRENT APPLICATION NUMBER: US/09/964,201A
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-201A-23

Query Match 44.0%; Score 22; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QCGDF 9
Db 1 RCGDY 5

RESULT 30
US-08-082-849B-15
Sequence 15, Application US/08082849B
Patent No. 5677274
GENERAL INFORMATION:
APPLICANT: Leppia, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Ariora, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
TITLE OF INVENTION: Related Methods
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B

FILING DATE: 25-JUN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-161-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Bacillus anthracis
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..12
OTHER INFORMATION: /label= PAHIV-2
US-08-082-849B-15

Query Match 44.0%; Score 22; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDF 9
Db 6 MMORGNF 12

RESULT 31
US-09-785-921A-13
Sequence 13, Application US/09785921A
Patent No. 6627197
GENERAL INFORMATION:
APPLICANT: Keener, William K.
APPLICANT: Ward, Thomas B.
TITLE OF INVENTION: SELECTIVE DESTRUCTION OF CELLS INFECTED WITH HUMAN
FILE REFERENCE: LIT-PI-529
CURRENT APPLICATION NUMBER: US/09/785,921A
CURRENT FILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 17
SEQ ID NO 13
LENGTH: 12
TYPE: PRT
ORGANISM: Human immunodeficiency virus
US-09-785-921A-13

Query Match 44.0%; Score 22; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGDF 9
Db 5 MMORGNF 11

RESULT 32
PCT-US94-01624-15
Sequence 15, Application PC/TUS9401624
GENERAL INFORMATION:
APPLICANT: Leppia, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Ariora, Naveen

APPLICANT: Singh, Yogendra
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
RELATED METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
STREET: Stewart Street Tower, 20th Floor, One Market
City: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01624
FILING DATE: June 25, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Bacillus anthracis
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..12
OTHER INFORMATION: /label= PAHIV-2
PCT-US94-01624-15
Query Match 44.0%; Score 22; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 5.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 MIOGDF 9
DB 6 MMORGNF 12
RESULT 33
US-07-847-743B-5
Sequence 5, Application US/07847743B
Patent No. 5367060
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
TITLE OF INVENTION: Structure, Production and Use of
NUMBER OF INVENTION: Heterogulin
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
City: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/847,743B
FILING DATE: 19920306
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-May-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-Sep-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-No. 5367060-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,043
REFERENCE/DOCKET NUMBER: 712P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-847-743B-5
Query Match 44.0%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 FMIOGD 8
DB 7 FAXVAGE 13
RESULT 34
US-08-036-555B-31
Sequence 31, Application US/08036555B
Patent No. 5530109
GENERAL INFORMATION:
APPLICANT: Goodheart, Andrew; Stroobant, Paul;
APPLICANT: Mungshetti, Luisa; Waterfield, Michael; Marchionni, Mark;
APPLICANT: Chen, Mao Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
NUMBER OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
City: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555B
FILING DATE: 24-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/840,389
FILING DATE: 03-SEP-1992

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Page 13

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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 5250.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-036-555B-31

Query Match      44.0%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      2 FMIQGD 8
DB      7 FCVNGGE 13

RESULT 35
US-08-469-569-31
Sequence 31, Application US/08469569
Patent No. 5606032
GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchionni, Mark;
APPLICANT: Chen, Mao Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
TITLE OF INVENTION: Preparation and Use
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felle & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,569
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 24-MAR-1993
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
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FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.K. 91 07566.3
FILING DATE: 10-APRIL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Tsai, Christine H.
REGISTRATION NUMBER: 34,266
REFERENCE/DOCKET NUMBER: LUD 5250.4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-469-569-31

Query Match      44.0%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY      2 FMIQGD 8
DB      7 FCVNGGE 13

RESULT 36
US-08-466-201-5
Sequence 5, Application US/08456201
Patent No. 5641869
GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.,
APPLICANT: Holmes, William E.
TITLE OF INVENTION: Structure, Production and Use of
TITLE OF INVENTION: Heregulin 2 Ligands
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,201
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,145
FILING DATE:
APPLICATION NUMBER: 07/880,917
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
ATTORNEY/AGENT INFORMATION:
NAME: Hensley, Max D.
REGISTRATION NUMBER: 27,034
REFERENCE/DOCKET NUMBER: 712P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/266-1489
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
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SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-456-201-5

Query Match 44.0%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIQGD 8
Db 7 FVNGGE 13

RESULT 37

US-08-249-322A-31
Sequence 31, Application US/08249322A

Patent No. 5716930

GENERAL INFORMATION:

APPLICANT: Goodheart, Andrew; Stroobant, Paul;

APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;

APPLICANT: Chen, Maio Su; Hiles, Ian

TITLE OF INVENTION: Glial Mitogenic Factors, Their

TITLE OF INVENTION: Preparation and Use

NUMBER OF SEQUENCES: 184

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Felte & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/249,322A

FILING DATE: 26-MAY-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/036,555

FILING DATE: 24-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/965,173

FILING DATE: 23-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/940,389

FILING DATE: 03-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/907,138

FILING DATE: 30-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/863,703

FILING DATE: 03-APRIL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.K. 91 07566.3

FILING DATE: 10-APRIL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Tsai, Christine H.

REGISTRATION NUMBER: 34,266

REFERENCE/DOCKET NUMBER: LUD 250.4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 688-3684

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 13

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-249-322A-31

Query Match 44.0%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIQGD 8
Db 7 FVNGGE 13

RESULT 38

US-08-469-526A-31

Sequence 31, Application US/08469526A

Patent No. 5792849

GENERAL INFORMATION:

APPLICANT: Goodheart, Andrew

APPLICANT: Stroobant, Paul

APPLICANT: Minghetti, Luisa

APPLICANT: Waterfield, Michael

APPLICANT: Marchioni, Mark

APPLICANT: Chen, Maio Su

APPLICANT: Hiles, Ian

TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR

TITLE OF INVENTION: PREPARATION AND USE

NUMBER OF SEQUENCES: 187

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Clark & Elding LLP

STREET: 176 Federal Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02110

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,526A

FILING DATE: 06 June 1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/036,555

FILING DATE: 24-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/965,173

FILING DATE: 23-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/940,389

FILING DATE: 03-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/907,138

FILING DATE: 03-JUN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/863,703

FILING DATE: 03-APRIL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.K. 91 07566.3

FILING DATE: 10-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bleker-Brady, Kristina

REGISTRATION NUMBER: 39,109

REFERENCE/DOCKET NUMBER: 04585/00200A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-428-0200

TELEFAX: 617-428-7045

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 13

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

Query Match 44.0%; Score 22; DB 1; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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QY 2 FMIOGCD 8
| : || :
Db 7 FXVNGGE 13

RESULT 39

US-08-330-161-5
; Sequence 5, Application US/08330161
; Patent No. 5834229

GENERAL INFORMATION:
APPLICANT: Vandlen, Richard
APPLICANT: Holmes, William
TITLE OF INVENTION: Structure, Production and Use of Heregulin 2 Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/330,161
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/035430
FILING DATE: 22-MAR-1993
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Carolyn R.
REGISTRATION NUMBER: 32,324
REFERENCE/DOCKET NUMBER: 712C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-2614
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-330-161-5

Query Match 44.0%; Score 22; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGCD 8
| : || :
Db 7 FXVNGGE 13

RESULT 40
US-08-456-241-5
; Sequence 5, Application US/08456241
; Patent No. 5840525

GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.
APPLICANT: Holmes, William E.
TITLE OF INVENTION: STRUCTURE, PRODUCTION AND USE OF
TITLE OF INVENTION: HERGULIN
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd

CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,241
FILING DATE: 31-MAY-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/126145
FILING DATE: 23-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/880917
FILING DATE: 11-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/847743
FILING DATE: 06-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/790801
FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/765212
FILING DATE: 25-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 712P4CID1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-08-456-241-5

Query Match 44.0%; Score 22; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 6.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGCD 8
| : || :
Db 7 FXVNGGE 13

RESULT 41
US-08-734-591A-31
; Sequence 31, Application US/08734591A
; Patent No. 5854220

GENERAL INFORMATION:
APPLICANT: Goodearl, Andrew
APPLICANT: Strobant, Paul
APPLICANT: Minchenti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Hiles, Ian
APPLICANT: Marchionni, Mark
APPLICANT: Chen, Mario
TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
TITLE OF INVENTION: PREPARATION AND USE
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Fling LLP
STREET: 176 Federal Street

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible Pentium
OPERATING SYSTEM: Windows95
SOFTWARE: Wordperfect (Version 7.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/734,591A
FILING DATE: 22-OCT-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/470,335
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/036,555
FILING DATE: 03-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/863,703
FILING DATE: 03-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 91 07566.3
FILING DATE: 10-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER: 39,109
REFERENCE/DOCKET NUMBER: 04585/00200P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 428-0200
TELEFAX: (617) 428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-734-591A-31
Query Match
Best Local Similarity 44.0%; Score 22; DB 2; Length 13;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 FMIOGD 8
Db 7 FCVNGE 13
RESULT 42
US-08-440-401-5
Sequence 5, Application US/08440401
Patent No. 5856110
GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.
TITLE OF INVENTION: Structure, Production and Use of
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,401
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330161
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/035430
FILING DATE: 22-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/705256
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 712C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-440-401-5
Query Match
Best Local Similarity 44.0%; Score 22; DB 2; Length 13;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 2 FMIOGD 8
Db 7 FCVNGE 13
RESULT 43
US-08-419-878B-5
Sequence 5, Application US/08419878B
Patent No. 5859206
GENERAL INFORMATION:
APPLICANT: Vandlen, Richard L.
TITLE OF INVENTION: Antibodies Specific For Heregulin 2-alpha
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,878B
FILING DATE: 11-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330161
FILING DATE: 25-OCT-1994

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/035430
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA: 07/705256
; APPLICATION NUMBER: 07/705256
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0712C2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-419-878B-5

Query Match
Best Local Similarity 44.0%; Score 22; DB 2; Length 13;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGD 8
DB 7 FCVNGE 13

RESULT 44
US-08-469-660-31
; Sequence 31, Application US/08469660
; Patent No. 5876973
; GENERAL INFORMATION:
; APPLICANT: Gwynne, David I.; Marchionni, Mark;
; APPLICANT: McBurney, Robert N.
; TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
; TITLE OF INVENTION: THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 184
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; ZIP: 0211-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,660
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/011,396
; FILING DATE: 23-JAN-1993
; PRIOR APPLICATION DATA: 07/994,085
; APPLICATION NUMBER: 07/994,085
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/951,747
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA: 07/927,337
; APPLICATION NUMBER: 07/927,337
; FILING DATE: 10-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/017004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: 200154
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; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
;
US-08-469-660-31

Query Match
Best Local Similarity 44.0%; Score 22; DB 2; Length 13;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGD 8
DB 7 FCVNGE 13

RESULT 45
US-08-470-335-31
; Sequence 31, Application US/08470335F
; Patent No. 6147190
; GENERAL INFORMATION:
; APPLICANT: GOODEARL, ANDREW
; APPLICANT: STROSBANT, PAUL
; APPLICANT: MINGHERTTI, LUISA
; APPLICANT: WATERFIELD, MICHAEL
; APPLICANT: MARCHIONNI, MARK
; APPLICANT: CHEN, MARIO S.
; APPLICANT: HILES, IAN
; TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
; TITLE OF INVENTION: PREPARATION AND USE
; RILE REFERENCE: 04585/00200B
; CURRENT APPLICATION NUMBER: US/08/470,335F
; CURRENT FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 08/036,555
; EARLIER FILING DATE: 1993-03-24
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-08-470-335-31

Query Match
Best Local Similarity 44.0%; Score 22; DB 3; Length 13;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FMIOGD 8
DB 7 FCVNGE 13

Search completed: August 30, 2004, 10:57:11
Job time : 5.55743 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:39:14 ; Search time 13.4068 Seconds
(without alignments)
189.646 Million cell updates/sec

Title: us-09-720-469a-2

Perfect score: 50

Sequence: 1 DPMIQQGDF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 309569

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq29Jan04:*

1: Geneseq19808:*\n2: Geneseq19908:*\n3: Geneseq20008:*\n4: Geneseq20018:*\n5: Geneseq20028:*\n6: Geneseq20038:*\n7: Geneseq2003bs:*\n8: Geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	100.0	9	3	AAV69922 Human cyc
2	50	100.0	9	4	AA846931 Human cyc
3	50	100.0	9	4	AA688089 Antitumou
4	50	100.0	9	5	ABG79076 Human Cyp
5	50	100.0	9	6	ABR84374 Human Cyp
6	50	100.0	9	7	ADCI7702 Cyclophil
7	47	94.0	9	3	AAV69963 Human cyc
8	47	94.0	9	4	AA846947 Human cyc
9	47	94.0	9	7	ADCI7709 Modified
10	44	88.0	9	3	AAV69958 Human cyc
11	39	78.0	9	3	AAV69957 Human cyc
12	39	78.0	14	5	ABG67616 Human ADP
13	39	78.0	14	6	ADA23375 Alzheimer
14	37	74.0	9	3	AAV69961 Human cyc
15	37	74.0	14	2	AAV69961 Human cyc
16	37	74.0	14	2	AAV69961 Human cyc
17	32	64.0	13	5	AAU1860 Monsanto
18	28	56.0	12	2	AAW1826 Mitochope
19	28	56.0	12	2	AAW1826 Mitochope
20	27	54.0	10	6	ABR5548 Amino aci
21	27	54.0	11	6	ADA18540 Human alp
22	27	54.0	12	6	ABU08824 Alpha fib
23	27	54.0	12	6	ABU09252 Human alp
24	27	54.0	13	6	ABU08825 Alpha fib
25	27	54.0	13	6	ABG76139 Human alp

26	27	54.0	13	6	ADA18539 Human alp
27	27	54.0	14	6	ABU08827 Alpha fib
28	26	52.0	9	2	AAV72938 E. coli p
29	26	52.0	9	2	AAV72938 E. coli p
30	26	52.0	10	2	AAV72949 E. coli p
31	26	52.0	10	2	AAV72905 E. coli p
32	26	52.0	12	2	AAW1441 HSV Glyco
33	26	52.0	12	3	AAV44921 Human sec
34	26	52.0	14	4	AAU68410 Human Bre
35	26	52.0	14	4	AAU68401 Human Bre
36	26	52.0	14	6	ABR75514 Liver res
37	25	50.0	9	2	AAV20729 Pancreas-
38	25	50.0	9	3	AAV51905 Elastase
39	25	50.0	9	4	AAW22987 HIV pep1
40	25	50.0	10	5	AAU78392 Biosurfac
41	25	50.0	14	4	AAV38171 Human SNP
42	24	48.0	8	2	AAV09052 Synthetic
43	24	48.0	8	3	AAV12089 Ad7 cel p
44	24	48.0	8	7	AAV84662 Adenoviru
45	24	48.0	9	2	AAV09051 Bsp-bind1

ALIGNMENTS

RESULT 1

AAV69922 standard; peptide: 9 AA.

11-APR-2000 (first entry)

Human cyclophilin B peptide fragment #2.

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;

HLA antigen; diagnosis; tumour; therapy.

Homo sapiens.

MO9967288-A1.

29-DEC-1999.

24-JUN-1999; 99WO-JP003360.

25-JUN-1998; 98JP-00178449.

(SUMU) SUMITOMO PHARM CO LTD.

(ITOH/) ITOH K.

Itoh K, Gomi S;

WPI; 2000-116932/10.

Claim 4; Page 49; 64pp; Japanese.

This sequence represents a cyclophilin B peptide of the invention. The

peptides are tumour antigen peptides derived from cyclophilin B, that

recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The

peptides are used for the treatment and diagnosis of tumours

Sequence 9 AA;

Query Match 100.0%; Score 50; DB 3; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 9; Conservative 0; Mismatches 0; Gaps 0;

1 DPMIQQGDF 9

PN WO200264057-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 15-FEB-2002; 2002WO-US005212.
 XX
 PR 15-FEB-2001; 2001US-0268687P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Wang R;
 DR WPI; 2002-627577/67.
 XX
 PT Novel composition for treating a disease in an animal, comprises an
 PT immune effector cell and cell penetrating peptide associated with an
 PT antigen or antibody.
 XX
 PS Disclosure; Page 17; 61pp; English.
 XX
 CC The invention relates to a composition (I) comprising an immune effector
 CC cell and a cell penetrating peptide (CPP) associated with an antigen or
 CC antibody. Also included are (1) a vaccine comprising (I), CPP associated
 CC with an antigen, and a pharmaceutically acceptable carrier and (2)
 CC preparing a composition for a disease, by providing (I) and CPP
 CC associated with an antigen for disease, and introducing the antigen-
 CC associated CPP to (I), where antigen enters into the cell. The antigens
 CC are, for example, tumour antigen derived epitopes recognised by tumour
 CC infiltrating lymphocytes (TIL) of HLA (human leukocyte antigen) class I
 CC or II. The composition is useful for enhancing immunity in an animal to a
 CC disease, by administering a mature dendritic cell comprising CPP
 CC associated with an antigen to disease, to the animal, such that following
 CC the administration, animal is protected from disease, where the animal
 CC comprises both CD4+ and CD8+ T cells. It is also useful for treating a
 CC disease (e.g. cancer, lymphoma, melanoma, thymoma, lymphoma, sarcoma, lung
 CC cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine
 CC cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma,
 CC breast cancer, prostate cancer, ovarian cancer and pancreatic cancer).
 CC The animal is further subjected to a cancer treatment including surgery,
 CC radiation, chemotherapy or gene therapy. The administration of (I),
 CC preferably dendritic cell is prior to, subsequent to or concurrent with,
 CC the cancer treatment. The present sequence is a tumour antigen derived
 CC epitope for inclusion in the composition of the invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFMIOGGDF 9
 Db 1 DFMIOGGDF 9
 XX
 XX
 XX
 XX
 XX
 DE Human CYPB HLA-A24 epitope, SEQ ID NO:24.
 XX
 XX
 AC ABR84374;
 XX
 AC ABR84374;
 XX
 XX
 DE Human CYPB HLA-A24 epitope, SEQ ID NO:24.
 XX
 XX
 KW Antigen specific T-cell; detection; diagnosis; cancer specific T-cell;
 KW cancer; tumour; cervical cancer; prostate cancer; cellular immunity;
 KW immune therapy; cytostatic; immunostimulant; vaccine; antigenic peptide;
 KW human leukocyte antigen; HLA-A24 epitope.
 XX
 OS Homo sapiens.
 XX
 PN JP2002365286-A.

XX
 PD 18-DEC-2002.
 XX
 PF 18-SEP-2001; 2001JP-00283413.
 XX
 PR 13-NOV-2000; 2000JP-00345094.
 XX
 PA (ITOY/) ITO Y.
 XX
 DR WPI; 2003-508315/48.
 XX
 PT A detection method of antigen specific T-cells, comprises the use of
 PT plural antigenic peptides, useful in semi-quantitative determination of
 PT cancer specific T-cell frequencies and for monitoring cellular immunity.
 XX
 PS Example 8; Page 10; 18pp; Japanese.
 XX
 CC The invention relates to a method for the detection of antigen specific T
 CC -cells in a blood sample involving the use of a plurality of antigenic
 CC peptides. The method comprises sampling of peripheral blood monocytes;
 CC stimulation of the collected peripheral blood monocytes with antigens
 CC without direct use of antigen presenting cells; and detection of T-cells
 CC specific to the antigen in the stimulated monocytes. The method is
 CC particularly used for the detection of cancer as it can be used in semi-
 CC quantitative determination of cancer specific T-cells. It can also be
 CC used for cancer vaccine therapy for patients with cervical or prostate
 CC cancer. The method can additionally be used to monitor of cellular
 CC immunity and cancer immune therapy by detection of specific T-cell
 CC frequencies. Sequences ABR84367-ABR84380 represent HLA-A24 (human
 CC leukocyte antigen) peptides of human origin used in an example from the
 CC invention
 XX
 SQ Sequence 9 AA;
 Query Match 100.0%; Score 50; DB 6; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DFMIOGGDF 9
 Db 1 DFMIOGGDF 9
 XX
 XX
 XX
 XX
 XX
 DE Cyclophilin B protein amino acids 91-99.
 XX
 XX
 KW cytoskeletal; antiallergic; vaccine; allergic reaction suppressor; antigen;
 KW allergy; epitope; cancer; immunoglobulin E antibody; desensitization;
 KW cyclophilin B.
 XX
 OS Synthetic.
 XX
 PN WO2003020306-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 28-AUG-2002; 2002WO-JP008641.
 XX
 PR 29-AUG-2001; 2001JP-00260046.
 XX
 PA (ITOH/) ITOH K.
 XX
 PI Itoh K, Yamada A;
 XX
 DR WPI; 2003-300831/29.
 XX

PT Desensitizers or allergic reaction suppressors containing peptides
 PT originating from the same antigenic substances as reaction-inducing
 PT substances, useful for preventing or treating type I allergic diseases
 PT and in cancer vaccines.

PS Claim 8; SEQ ID NO 2; 43pp; Japanese.

XX
 CC The invention relates to allergic reaction suppressors, comprising a
 CC peptide which originates from the same antigenic substance as the
 CC antigenic substance inducing the (peptide-originated) allergic reaction,
 CC and containing an epitope different from the epitope participating in the
 CC induction of the allergic reaction and yet does not induce the allergic
 CC reaction. The desensitizers or allergic reaction suppressors are useful
 CC for treating and preventing type I allergic diseases and in cancer
 CC vaccines for preventing or treating cancer. The allergic reaction
 CC suppressors are also useful for suppressing an allergic reaction or
 CC reducing immunoglobulin E antibody production, and for desensitization to
 CC antigens. This sequence represents a peptide used in the invention and
 CC corresponds to amino acids 91-99 of the cyclophilin B protein.

XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 50; DB 7; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFMIOGDP 9
 1 DFMIOGDP 9

DB 1 DFMIOGDP 9

RESULT 7
 AA69963
 ID AA69963 standard; peptide; 9 AA.

XX
 AC AA69963;

XX 11-APR-2000 (first entry)

XX
 DE Human cyclophilin B peptide fragment #43.

XX
 KM Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
 KM HLA antigen; diagnosis; tumour therapy.

XX
 OS Homo sapiens.

XX
 PN WO967288-A1.

XX 29-DEC-1993.

XX PD 24-JUN-1999; 99WO-0P003360.

XX PF 25-JUN-1998; 98JP-00178449.

XX PR (SUMU) SUMITOMO PHARM CO LTD.

XX PA (ITOH/) ITOH K.

XX PI Itoh K, Gomi S;

XX
 DR WPI; 2000-116932/10.

XX
 PT Tumor antigen peptides derived from cyclophilin B for treatment and
 PT diagnosis of tumors.

XX
 PS Claim 10; Page 60; 64pp; Japanese.

XX
 CC This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumor antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours

XX
 SQ Sequence 9 AA;

Query Match 94.0%; Score 47; DB 3; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFMIOGDP 9
 1 DFMIOGDP 9

DB 1 DFMIOGDP 9

RESULT 8
 AAB46947
 ID AAB46947 standard; peptide; 9 AA.

XX
 AC AAB46947;

XX
 DT 04-MAY-2001 (first entry)

XX
 DE Human cyclophilin B derived tumor antigenic peptide SEQ ID 33.

XX
 KM Tumor antigenic peptide; interferon; IFN; antigen-specific T cell;
 KM virucide; cytostatic; gene therapy; IFN-alpha; cytotoxic T cell;
 KM viral infectious disease; cyclophilin B; human.

XX
 OS Homo sapiens.

XX
 PN EP1074267-A1.

XX PD 07-FEB-2001.

XX PF 24-JUL-2000; 2000EP-00306263.

XX PR 22-JUL-1999; 99JP-00207687.

XX
 PA (SUMU) SUMITOMO PHARM CO LTD.

XX
 PI Takasu H, Gotoh M, Yamaoka T;

XX
 DR WPI; 2001-193144/20.

XX
 PT Use of antigenic proteins, peptides, interferon or their encoding DNA, in
 PT the manufacture of an agent for the induction of antigen-specific T
 PT cells.

XX
 PS Disclosure; Page 20; 25pp; English.

XX
 CC This invention describes the novel use of interferons (IFNs) or DNAs
 CC capable of expressing the interferons and/or antigenic proteins (AP),
 CC antigenic peptides derived from the proteins or DNAs capable of
 CC expressing the antigenic proteins or peptides, in the manufacture of an
 CC agent for induction of antigen-specific T cells. The products of the
 CC invention have virucide and cytostatic activity and can be used for gene
 CC therapy or as inducers of antigen-specific T cells. The action of
 CC interferon-alpha (IFN-alpha) in a system for inducing specific cytotoxic
 CC T cell (CTL) by administering an antigenic peptide in an incomplete
 CC Freund's adjuvant (IFA) emulsion preparation form was evaluated. IFNs (or
 CC DNA encoding IFNs) are useful in the manufacture of a medicament for
 CC inducing antigen-specific T cells in an individual who has been
 CC administered with AP (or DNA encoding AP) or vice versa. The medicament
 CC is useful for the treatment or prophylaxis of a tumor or a viral
 CC infectious disease

XX
 SQ Sequence 9 AA;

Query Match 94.0%; Score 47; DB 4; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.4e+06;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 DFMIOGDP 9
 1 DFMIOGDP 9

DB 1 DFMIOGDP 9

RESULT 9

ID	ADCl17709	standard; peptide; 9 AA.
XX	ADCl17709	
AC	ADCl17709;	
XX		
DT	18-DEC-2003	(First entry)
XX		
DE	Modified cyclophilin B protein amino acids 91-99.	
XX		
KM	Cycrostatic; antiallergic; vaccine; allergic reaction suppressor; antigen;	
KW	allergy; epitope; cancer; immunoglobulin E antibody; desensitization;	
KM	cyclophilin B.	
OS	Synthetic.	
XX		
FN	WO2003020306-A1.	
PD	13-MAR-2003.	
XX		
PF	28-AUG-2002; 2002WO-JP008641.	
XX		
PR	29-AUG-2001; 2001JP-00260046.	
XX		
PA	(ITOH/) ITOH K.	
P1	Itoh K, Yamada A;	
XX		
DR	WPI; 2003-300831/29.	
XX		
PT	Desensitizers or allergic reaction suppressors containing peptides	
PT	originating from the same antigenic substances as reaction-inducing	
PT	substances, useful for preventing or treating type I allergic diseases	
PT	and in cancer vaccines.	
PS		
FS	Claim 8; SEQ ID NO 9; 49pp; Japanese.	
XX		
CC	The invention relates to allergic reaction suppressors, comprising a	
CC	peptide which originates from the same antigenic substance as the	
CC	antigenic substance inducing the (peptide-originated) allergic reaction,	
CC	and containing an epitope different from the epitope participating in the	
CC	induction of the allergic reaction and yet does not induce the allergic	
CC	reaction. The desensitizers or allergic reaction suppressors are useful	
CC	for treating and preventing type I allergic diseases and in cancer	
CC	vaccines for preventing or treating cancer. The allergic reaction	
CC	suppressors are also useful for suppressing an allergic reaction or	
CC	reducing immunoglobulin E antibody production, and for desensitization to	
CC	antigens. This sequence represents a peptide used in the invention and	
CC	corresponds to amino acids 91-99 of the cyclophilin B protein with the	
CC	Phe at position 92 replaced by a Tyr.	
XX		
SQ	Sequence 9 AA;	
QY		
DB	Query Match	94.0%; Score 47; DB 7; Length 9;
	Best Local Similarity	88.9%; Pred. No. 1.4e+06;
	Matches 8; Conservative	1; Mismatches 0; Indels 0; Gaps 0
	1 DFMIOGSDP 9	
	.:	
	1 DYMIQGSDP 9	
RESULT 10		
ID	AAV69958	
AC	AAV69958 standard; peptide; 9 AA.	
XX		
XX	AAV69958;	
DT	11-APR-2000	(First entry)
XX		
DE	Human cyclophilin B peptide fragment #38.	
XX		
KM	Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;	
KW	HLA antigen; diagnosis; tumour; therapy.	

```

XX      Homo sapiens.
OS
XX      WO9967288-A1.
XX      29-DEC-1999.
XX      24-JUN-1999; 99WO-JP003360.
XX      25-JUN-1998; 98JP-00178449.
XX      (SUMU ) SUMITOMO PHARM CO LTD.
XX      (ITOH/) ITOH K.
XX      Itoh K, Gomi S;
XX      WPI; 2000-116932/10.
XX      Tumor antigen peptides derived from cyclophilin B for treatment and
XX      diagnosis of tumors.
XX      Claim 4; Page 61; 64pp; Japanese.
XX      This sequence represents a cyclophilin B peptide of the invention. The
XX      peptides are tumor antigen peptides derived from cyclophilin B, that
XX      recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
XX      peptides are used for the treatment and diagnosis of tumours
XX      Sequence 9 AA:
SQ
XX      Query Match 88.0%; Score 44; DB 3; Length 9;
XX      Best Local Similarity 100.0%; Pred. NO. 1.4e+06;
XX      Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
CY      1 DFMIOGCD 8
XX      1 DFMIOGCD 8
DB
XX      1 DFMIOGCD 8
XX
XX      RESULT 11
XX      ID AAY69957
XX      ID AAY69957 standard; peptide; 9 AA.
XX      AC AAY69957;
XX      DT 11-APR-2000 (first entry)
XX      DE Human cyclophilin B peptide fragment #37.
XX      KW Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL;
XX      HLA antigen; diagnosis; tumour; therapy.
XX      OS Homo sapiens.
XX      PN WO9967288-A1.
XX      PD 29-DEC-1999.
XX      PF 24-JUN-1999; 99WO-JP003360.
XX      PR 25-JUN-1998; 98JP-00178449.
XX      (SUMU ) SUMITOMO PHARM CO LTD.
XX      (ITOH/) ITOH K.
XX      Itoh K, Gomi S;
XX      WPI; 2000-116932/10.
XX      Tumor antigen peptides derived from cyclophilin B for treatment and
XX      diagnosis of tumors.
XX      Claim 4; Page 61; 64pp; Japanese.

```

XX This sequence represents a cyclophilin B peptide of the invention. The
 CC peptides are tumor antigen peptides derived from cyclophilin B, that
 CC recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The
 CC peptides are used for the treatment and diagnosis of tumours
 XX
 SQ Sequence 9 AA;

Query Match 78.0%; Score 39; DB 3; Length 9;
 Best Local Similarity 87.5%; Pred. No. 14e+06;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIGGDF 9
 DB 2 FMCGGDF 9

RESULT 12
 ABG67616
 ID ABG67616 standard; peptide; 14 AA.

AC ABG67616;

DT 07-OCT-2002 (first entry)

DE Human ADPI tryptic digest peptide #325.

XX Human; Alzheimer's disease; AD; brain tissue; ADF; ADPI;

KW Alzheimer's disease-associated feature; neuroprotective;

KM Alzheimer's disease-associated protein isoform; nootropic;

XX ADPI tryptic digest peptide.

OS Homo sapiens.

PN WO200246767-A2.

XX 13-JUN-2002.

PF 29-NOV-2001; 2001WO-GB005289.

PR 08-DEC-2000; 2000US-0254431P.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

XX Herath HMAc, Parekh RB, Rohlf C;

DR WPI; 2002-508575/54.

XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT comprises detecting Alzheimer disease-associated features or Alzheimer
 PT disease-associated protein isoforms in brain tissue from the subject.
 XX
 PS Claim 7; Page 72; 427pp; English.

XX The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of Alzheimer's disease (AD) in a
 CC subject. The method comprises analysing a sample of brain tissue from a
 CC subject by 2D electrophoresis to generate a 2D array of Alzheimer's
 CC disease-associated features (ADFs), whose relative abundance correlates
 CC with the presence, absence, stage or severity of AD and comparing the
 CC abundance of each feature with the abundance of that chosen feature in
 CC brain tissue from persons free from AD. The invention also describes
 CC Alzheimer's disease-associated protein isoforms (ADPIs) detectable in
 CC brain tissue. The methods and compositions of the invention are useful
 CC for the screening, diagnosis or prognosis of AD in a subject, for
 CC determining the stage or severity of AD in a subject, for identifying a
 CC subject at risk of developing AD, or for monitoring the effect of therapy
 CC administered to a subject having AD. Antibodies capable of binding to
 CC ADPIs are useful for treating or preventing AD, and for determining the
 CC efficacy of a given treatment regime. An agent that modulates the
 CC activity of ADPI is useful in the manufacture of a medicament for the
 CC treatment or prevention of AD in a subject. ABG67292-ABG68038 represent
 CC human ADPI tryptic digest peptides

XX SQ Sequence 14 AA;

Query Match 78.0%; Score 39; DB 5; Length 14;
 Best Local Similarity 87.5%; Pred. No. 3.1;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIGGDF 9
 DB 5 FMCGGDF 12

RESULT 13
 ADA23735
 ID ADA23735 standard; peptide; 14 AA.

AC ADA23735;

DT 20-NOV-2003 (first entry)

DE Alzheimer's disease-associated protein isoform tryptic peptide #344.

XX human; Alzheimer's disease; vascular dementia; Lewy body dementia;

KW schizophrenia; Parkinson's disease; multiple sclerosis; depression;

KM Alzheimer's disease-associated protein isoform; ADPI.

XX Homo sapiens.

PN US2003064411-A1.

XX 10-DEC-2001; 2001US-00014340.

PR 08-DEC-2000; 2000US-0254431P.

PA (HERA/) HERATH H M A C.

PA (PARE/) PAREKH R B.

XX (ROHL/) ROHLF C.

PI Herath HMAc, Parekh RB, Rohlf C;

DR WPI; 2003-540784/51.

XX Screening, diagnosis or prognosis of Alzheimer's disease in subject,
 PT involves analyzing test sample of brain tissue from subject, and
 PT comparing feature in test sample with that of person(s) free from
 PT Alzheimer's disease.
 XX
 PS Disclosure; SEQ ID NO 344; 115pp; English.

XX The invention relates to a method of screening or diagnosing Alzheimer's
 CC disease in a subject. The method is useful for screening, diagnosis or
 CC prognosis of Alzheimer's disease in a subject for determining the stage
 CC of severity of Alzheimer's disease in a subject, for identifying a
 CC subject at risk of developing Alzheimer's disease, or for monitoring the
 CC effect of therapy administered to a subject having Alzheimer's disease.
 CC The method is also useful in treating vascular dementia, Lewy body
 CC dementia, schizophrenia, Parkinson's disease, multiple sclerosis or
 CC depression. The inventive method identifies sensitive and specific
 CC biomarkers for the diagnosis of Alzheimer's disease in living subjects.
 CC It provides therapeutic agents for Alzheimer's disease that works
 CC quickly, potentially, specifically with fewer side effects. The present
 CC sequence represents the amino acid sequence of a Alzheimer's disease-
 CC associated protein isoform tryptic peptide.

XX SQ Sequence 14 AA;

Query Match 78.0%; Score 39; DB 6; Length 14;
 Best Local Similarity 87.5%; Pred. No. 3.1;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIGGDF 9

Db 5 FMIOGDF 12

RESULT 14
AA69961
ID AA69961 standard; peptide; 9 AA.

AA69961;

11-APR-2000 (first entry)

Human cyclophilin B peptide fragment #41.

Cyclophilin B; human; tumour antigen peptide; cytotoxic T-cell; CTL; HLA antigen; diagnosis; tumour; therapy.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 2 /label= Phe, Tyr, Met, Trp

Misc-difference 9 /label= Phe, Leu, Ile, Trp, Met

WO9967288-A1.

29-DEC-1999.

24-JUN-1999; 99WO-JP003360.

25-JUN-1998; 98JP-00178449.

(SUNU) SUMITOMO PHARM CO LTD.

(ITOH/) ITOH K.

Itoh K, Gomi S;

WPI; 2000-116932/10.

Tumor antigen peptides derived from cyclophilin B for treatment and diagnosis of tumors.

Claim 10; Page 60; 64pp; Japanese.

This sequence represents a cyclophilin B peptide of the invention. The peptides are tumour antigen peptides derived from cyclophilin B, that recognise cytotoxic T-cells (CTL) which bind to the HLA antigen. The peptides are used for the treatment and diagnosis of tumours

Sequence 9 AA;

Query Match 74.0%; Score 37; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 1.4e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FMIOGDF 8
Db 1 FMIOGDF 8

RESULT 15
AA72947
ID AA72947 standard; peptide; 14 AA.

AA72947;

16-OCT-2003 (revised)
25-MAR-2003 (revised)
29-NOV-1995 (first entry)

E. coli PPIase-alpha tryptic fragment 4.

Escherichia coli; protein conformation; folding; acceleration;
PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
isomerisation; prolyl peptide bond.

Escherichia coli; (ST 249 strain).

EP647714-A1.

12-APR-1995.

19-JUL-1990; 94EP-00203612.

19-JUL-1989; 89JP-00184738.
06-OCT-1989; 89JP-00260244.
29-DEC-1989; 89JP-00344705.
19-JUL-1990; 90EP-00307914.

(TOFU) TONEN CORP.

Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;

WPI; 1995-140756/19.

New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate the folding of proteins, partic. for activation of inactive recombinant proteins.

Example 7; Page 30; 85pp; English.

AA72945-48 are tryptic fragments of E. coli PPIase-alpha (peptidyl prolyl cis trans isomerase). The E. coli PPIase-beta has a single mol. wt. of about 22 kDa and a single isoelectric point of about 9.7. The enzyme catalyses the isomerisation of prolyl peptide bonds in proteins and accelerates the folding of the protein. The inventors are claiming a PPIase-beta. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 16-OCT-2003 to standardise OS field)

Sequence 14 AA;

Query Match 74.0%; Score 37; DB 2; Length 14;
Best Local Similarity 87.5%; Pred. No. 6.3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FMIOGDF 9
Db 5 FMIOGDF 12

RESULT 16
AA72903
ID AA72903 standard; peptide; 14 AA.

AA72903;

16-OCT-2003 (revised)
25-MAR-2003 (revised)
29-NOV-1995 (first entry)

E. coli PPIase-alpha tryptic fragment 4.

Escherichia coli; protein conformation; folding; acceleration;
PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
isomerisation; prolyl peptide bond.

Escherichia coli; (ST 249 strain).

EP647713-A1.
12-APR-1995.

19-JUL-1990; 94EP-00203610.

PR 19-JUL-1989; 89JP-00184738.
 PR 06-OCT-1989; 89JP-00260244.
 PR 29-DEC-1989; 89JP-00344705.
 PR 19-JUL-1990; 90BP-00307914.
 XX
 PA (TOFU) TONEN CORP.
 XX
 PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
 DR WPI; 1995-140755/19.
 XX
 PT New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate
 PT the folding of proteins, partic. for activation of inactive recombinant
 PT proteins.
 PS Example 7; Page 30; 85pp; English.
 XX
 CC AAR72900-04 are tryptic fragments of E. coli Ppiase-alpha (peptidyl
 CC prolyl cis trans isomerase). The E. coli Ppiase-beta has a single mol.
 CC wt. of about 22 kDa and a single isoelectric point of about 9.7. The
 CC enzyme catalyzes the isomerisation of prolyl peptide bonds in proteins
 CC and accelerates the folding of the protein. The inventors are claiming
 CC the Ppiase-alpha. (Updated on 25-MAR-2003 to correct PN field.) (Updated
 CC on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
 CC PR field.) (Updated on 16-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 14 AA;
 Query Match 74.0%; Score 37; DB 2; Length 14;
 Best Local Similarity 87.5%; Pred. No. 6; 9;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FMIQGGDF 9
 Db 5 FMIQGGGF 12
 RESULT 17
 AAU81860
 ID AAU81860 standard; peptide; 13 AA.
 AC AAU81860;
 XX
 DT 09-APR-2002 (first entry)
 DE Monsanto Bacillus thuringiensis (MONT) antigenic peptide #16.
 DE
 XX Antibody; protease cleavage map; genetically modified organism; BT;
 KM cryIA; cryIIA; insect resistance; transgenic plant.
 XX
 OS Bacillus thuringiensis.
 OS Synthetic.
 XX
 PN WO200198523-A2.
 XX
 PD 27-DEC-2001.
 PF 20-JUN-2001; 2001WO-KR001054.
 XX
 PR 20-JUN-2000; 2000KR-00033931.
 PR 20-JUN-2001; 2001KR-00035066.
 XX
 PA (GDBI-) GD BIOTECH CO LTD.
 XX
 PI Park H;
 DR WPI; 2002-122286/16.
 XX
 PT Novel antibody useful for detecting foodstuff made from genetically
 PT modified organism, combines specifically with synthetic peptides prepared
 PT from protease-digested recombinant proteins specific for transgenic
 PT plant.
 XX

PS Claim 7; Page 12; 36pp; English.
 XX
 CC The invention describes an antibody which combines specifically with
 CC recombinant protein. It is prepared by analysing a protease cleavage map
 CC of the recombinant protein expressed in genetically modified organism.
 CC Peptides are selected from the same cleavage map and used to create
 CC synthetic peptides used for preparing the antibodies. The antibody is
 CC useful for detecting a foodstuff (a plant or processed food) prepared
 CC from a genetically modified organism which involves reacting the antibody
 CC with a foodstuff and confirming an antigen-antibody reaction to
 CC distinguish foodstuff prepared from wild-type plant from foodstuff
 CC prepared from genetically modified organism. This sequence represents a
 CC peptide derived from Bacillus thuringiensis (BT) cryIA and cryIIA genes,
 CC which induce resistance to harmful insects. This peptide is used to
 CC create a synthetic peptide for the production of an antibody used to
 CC detect BT in insect resistant plants, described in the method of the
 CC invention
 XX
 SQ Sequence 13 AA;
 Query Match 64.0%; Score 32; DB 5; Length 13;
 Best Local Similarity 75.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DFMIQGGD 8
 Db 4 DFIIQGGD 11
 RESULT 18
 AAM32696
 ID AAM32696 standard; peptide; 12 AA.
 AC AAM32696;
 XX
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 DE
 XX Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KM monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KM platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KM anti thrombotic drug; ristocetin.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9718236-A1.
 XX
 PD 22-MAY-1997.
 XX
 PF 08-NOV-1996; 96WO-US017882.
 XX
 PR 13-NOV-1995; 95US-00556597.
 XX
 PA (UNY) UNIV NEW YORK STATE RES FOUND.
 XX
 PI Miller JL, Lyle VA;
 DR WPI; 1997-289227/26.
 XX
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex epitope -
 PT also anti-mimotope molecule capable of binding to the peptide and useful
 PT to modulate platelet adhesion, aggregation or agglutination.
 XX
 PS Claim 3; Page 98; 115pp; English.
 XX
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (MAb) which recognises an epitope
 CC within the human platelet glycoprotein (GP) Ib/IX complex. More
 CC specifically the MAb is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise

CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits the
 CC ristocetin induced aggregation of platelets

XX
 SQ Sequence 12 AA;

Query Match 56.0%; Score 28; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIOGDF 9
 |::|||
 1 FVVRGGTF 8

RESULT 19
 AAW71826
 ID AAW71826 standard; peptide; 12 AA.

XX AAW71826;
 XX
 DT 08-DEC-1998 (first entry)

XX Mimotope capable of binding to monoclonal antibody C-34 #75.

XX Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 XX binding site; Platelet epitope; neutralise; aggregation; inhibition;
 XX von Willebrand factor interaction; adhesion; agglutination.

XX Synthetic.

XX Homo sapiens.

XX US5817748-A.

XX 06-OCT-1998.

XX 17-MAR-1995; 95US-00406330.

XX 17-MAR-1995; 95US-00406330.

XX (UNIV) UNIV NEW YORK STATE RES FOUND.

XX Miller JL, Lyle VA;

XX WPI; 1998-556458/47.

XX Peptides that mimic platelet epitope - and neutralise aggregation-

XX inhibiting antibody.

XX Disclosure; Col 6; 26pp; English.

XX The present invention provides peptides which functionally mimic a
 XX binding site for a monoclonal antibody, where the monoclonal antibody
 XX recognises an epitope within the human glycoprotein Ib/IX complex.

XX Peptides AAW71752 to AAW71832 are mimotopes which are capable of binding
 XX to monoclonal antibody C-34. The invention also provides an isolated
 XX molecule capable of binding the mimotopes, where the molecule can be an
 XX antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 XX molecule, or other naturally or chemically synthesised molecules. These
 XX molecules are called anti-mimotopes and can act as anti-thrombotic drugs.

XX A method has also been described for modulating the adhesion,
 XX aggregation, or agglutination of platelets, where the method comprises
 XX selecting platelets and exposing them to an anti-mimotope molecule. The
 XX exposure affects von Willebrand factor interaction with platelets through
 XX the glycoprotein Ib/IX receptor, which modulates the adhesion,
 XX aggregation, or agglutination of the platelets. The peptide mimotopes
 XX mimic platelet epitopes

XX Sequence 12 AA;

Query Match 56.0%; Score 28; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 FMIOGDF 9
 |::|||
 1 FVVRGGTF 8

RESULT 20
 ABR55548
 ID ABR55548 standard; protein; 10 AA.

XX ABR55548;
 XX
 DT 11-AUG-2003 (first entry)

XX Amino acid sequence of a fragment of fibrinopeptide A.

XX Protein C; thrombin; fibrinopeptide A; serine protease; antithrombotic;

XX antiinflammatory; antiapoptotic; profibrinolytic;

XX hypercoagulable disease; thrombosis; myocardial infarction;

XX pulmonary embolism; reocclusion; angioplasty; thrombomodulin.

XX Homo sapiens.

XX FR2831170-A1.

XX 25-APR-2003.

XX 19-OCT-2001; 2001FR-00013492.

XX 19-OCT-2001; 2001FR-00013492.

XX (INRM) INSERM INST NAT SANTE & RECH MEDICALE.

XX Le Bornec B, Marque PE, Louvain V, Caimel C, Bianchini E;

XX Alach M;

XX WPI; 2003-451127/43.

XX New chimeric protein, cleavable by thrombin, useful e.g. as

XX antithrombotic agents, particularly modified protein C containing

XX artificial activation sequence.

XX Disclosure; Page 9; 51pp; French.

XX The present sequence represents a peptide, derived from fibrinopeptide A.
 XX The specification describes a chimeric protein, based on protein C, which
 XX comprises a thrombin-cleavable artificial sequence. This artificial
 XX sequence is of a formula given in the specification, and comprises a
 XX peptide from fibrinopeptide A, and a thrombin-cleavage site, other than
 XX that of the alpha-chain of fibrinogen. The chimeric protein and serine
 XX protease derivatives obtained by cleaving the chimeric protein with
 XX thrombin, are useful as antithrombotic, antiinflammatory, antiapoptotic
 XX and profibrinolytic agents, for treatment or prevention of
 XX hypercoagulable diseases, e.g. venous and arterial thrombosis;
 XX myocardial infarction; pulmonary embolism; reocclusion after angioplasty
 XX and alterations in the genes for protein C and thrombomodulin

XX Sequence 10 AA;

Query Match 54.0%; Score 27; DB 6; Length 10;
 Best Local Similarity 57.1%; Pred. No. 2.7e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DFMIOG 7
 |::|||
 1 DFLAEGG 7

RESULT 21

ADA18540
 ID ADA18540 standard; peptide; 11 AA.

PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
DR WPI; 2003-370707/35.
XX
XX
XX Novel biopolymer marker useful for indicating a particular disease state,
PT e.g. renal failure, comprises a peptide sequence of 12 amino-acids.
PS Claim 1; Page 7; 10pp; English.
XX
XX The invention relates to a biopolymer marker useful for indicating at
CC least one particular disease state e.g. renal failure. The biopolymer
CC marker is useful for developing diagnostic test to identify asymptomatic
CC patients before they suffer an irreversible event. The biopolymer marker
CC enables a diagnostician to gain the ability to characterise either the
CC presence or absence of the at least one disease state relative to the
CC recognition of the presence or absence of the biopolymer. The marker may
CC be of particular use in early diagnosis of Syndrome X, a multi-faceted
CC disease characterised by insulin resistance, dyslipidaemia, hypertension,
CC obesity and non-insulin dependent diabetes. The present sequence is the
CC biopolymer marker of the invention being a peptide derived from human
CC alpha fibrinogen
XX
SQ Sequence 12 AA;

Query Match 54.0%; Score 27; DB 6; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
||: ||
Db 3 DFLAEGG 9

RESULT 24
AB008825
ID AB008825 standard; peptide; 13 AA.
XX
XX AC AB008825;
XX
XX DT 25-AUG-2003 (first entry)
XX
XX DE Alpha fibrinogen peptide; #2, used for myocardial infarction diagnostics.
XX
XX KW Proteomic; human; physiological condition; analyte; biopolymer;
XX biomarker; alpha fibrinogen; myocardial infarction; MI.
XX
XX OS Homo sapiens.
XX
XX PN US2002160420-A1.
XX
XX PD 31-OCT-2002.
XX
XX PF 30-APR-2001; 2001US-00846330.
XX
XX PR 30-APR-2001; 2001US-00846330.
XX
XX PA (JACK/) JACKOWSKI G.
XX (THAT/) THATCHER B.
XX (MARS/) MARSHALL J.
XX (YANT/) YANTHA J.
XX (VREE/) VREES T.
XX
XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
XX DR WPI; 2003-491923/46.
XX
XX PT Determining proteomic basis e.g. basis for diagnosing existence of or
PT predicting development and/or progression of abnormal physiological
PT conditions based upon the presence of proteomic materials.

XX
XX Disclosure; Page 10; 25pp; English.
XX
XX The invention discloses a method for determining a proteomic basis for
CC development and progression of abnormal physiological conditions. The
CC method comprises isolating one or more patient specific proteomic
CC materials from a sample and comparing it against a library of proteomic
CC materials having characteristics identifiable with both normal and
CC abnormal physiological conditions or their predictive hallmarks. The
CC method is useful for determining a proteomic basis for development and
CC progression of abnormal physiological conditions. The method is also
CC useful for evaluating samples containing several analyses/biopolymers for
CC the presence of physiological condition specific sequences. The peptide
CC presented is a biomarker from alpha fibrinogen and is associated with
XX myocardial infarction (MI)
XX
SQ Sequence 13 AA;

Query Match 54.0%; Score 27; DB 6; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFMIOGG 7
||: ||
Db 3 DFLAEGG 9

RESULT 25
ABG76139
ID ABG76139 standard; peptide; 13 AA.
XX
XX AC ABG76139;
XX
XX DT 08-MAY-2003 (first entry)
XX
XX DE Human alpha fibrinogen peptide #2.
XX
XX KW Human; alpha fibrinogen; renal failure; myocardial infarction;
XX unstable angina; matrix assisted laser desorption-time of flight;
XX MALDI-TOF; mass spectroscopy; antigen.
XX
XX OS Homo sapiens.
XX
XX PN US2002160528-A1.
XX
XX PD 31-OCT-2002.
XX
XX PF 30-APR-2001; 2001US-00845729.
XX
XX PR 30-APR-2001; 2001US-00845729.
XX
XX PA (JACK/) JACKOWSKI G.
XX (THAT/) THATCHER B.
XX (MARS/) MARSHALL J.
XX (YANT/) YANTHA J.
XX (VREE/) VREES T.
XX
XX PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
XX DR WPI; 2003-255194/25.
XX
XX PT Novel biopolymer marker such as alpha fibrinogen having specific
PT molecular weight, useful in indicating disease state such as myocardial
PT infarction or renal failure.
XX
XX PS Claim 1; Page 7; 10pp; English.
XX
XX The invention relates a biopolymer marker such as alpha fibrinogen having
CC a molecular weight of about 1350 daltons and a sequence appearing as
CC ABG76139 useful in indicating at least one particular disease state. The
CC presence of the peptide in a sample is determined by matrix assisted
CC laser desorption-time of flight (MALDI-TOF) mass spectroscopy. The marker
CC is useful for indicating at least one particular disease state such as

CC myocardial infarction or renal failure (e.g. in a patient presenting with
 CC unstable angina). The biopolymer marker is useful as antigen in
 CC immunoassays for the detection of those individuals suffering from the
 CC disease known to be evidenced by the marker sequence. The biopolymer
 CC marker rapidly and accurately diagnoses a disease state such as
 CC myocardial infarction or renal failure, and allows physicians to identify
 CC asymptomatic patients before they suffer from the disease state. The
 CC present sequence is an alpha fibrinogen biopolymer marker

XX
 SQ Sequence 13 AA;

Query Match 54.0%; Score 27; DB 6; Length 13;
 Best Local Similarity 57.1%; Pred. No. 3.6e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPMIOGG 7
 ||: ||
 Db 4 DFLABCG 10

RESULT 26

ADA18539
 ID ADA18539 standard; peptide; 13 AA.

XX
 AC ADA18539;

XX
 DT 20-NOV-2003 (first entry)

XX
 DE Human alpha fibrinogen peptide #1.

XX
 KW Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;

XX
 KW surfaces enhanced for laser desorption/ionisation.

OS Homo sapiens.

XX
 PN US2002160422-A1.

XX
 PD 31-OCT-2002.

XX
 PF 30-APR-2001; 2001US-00846342.

XX
 PR 30-APR-2001; 2001US-00846342.

XX
 PA (JACK/) JACKOWSKI G.

PA (THAT/) THATCHER B.

PA (MARS/) MARSHALL J.

PA (YANT/) YANTHA J.

PA (VREE/) VREES T.

XX
 PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;

XX
 DR WPI; 2003-219986/21.

XX
 PT Novel biopolymer marker useful in indicating disease state, in particular

XX
 PT myocardial infarction.

XX
 PS Disclosure; Fig 1; 10pp; English.

CC The invention relates to a biopolymer marker useful in indicating at
 CC least one particular disease state. This marker is characterised as alpha
 CC fibrinogen having a molecular weight of 1077 Daltons and is useful for
 CC indicating a disease state, in particular myocardial infarction. The
 CC marker sequences are useful as antigens in immunoassays for the detection
 CC of those individuals suffering from the disease known to be evidenced by
 CC the marker sequence. The marker provides an efficient diagnostic tool for
 CC rapidly and accurately diagnosing disease states such as myocardial
 CC infarction. The marker was detected by the technique of surfaces enhanced
 CC for laser desorption/ionisation (SELDI) mass spectroscopy. The present
 CC sequence is the detected alpha fibrinogen marker peptide.

XX
 SQ Sequence 13 AA;

Query Match

54.0%; Score 27; DB 6; Length 13;

Best Local Similarity 57.1%; Pred. No. 3.6e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPMIOGG 7
 ||: ||
 Db 3 DFLABCG 9

RESULT 27

ABU08827
 ID ABU08827 standard; peptide; 14 AA.

XX
 AC ABU08827;

XX
 DT 25-AUG-2003 (first entry)

XX
 DE Alpha fibrinogen peptide, #3, used for renal failure diagnostics.

XX
 KW Proteomic; human; physiological condition; analyte; biopolymer;

XX
 KW biomarker; alpha fibrinogen; renal failure.

OS Homo sapiens.

XX
 PN US2002160420-A1.

XX
 PD 31-OCT-2002.

XX
 PF 30-APR-2001; 2001US-00846330.

XX
 PR 30-APR-2001; 2001US-00846330.

XX
 PA (JACK/) JACKOWSKI G.

PA (THAT/) THATCHER B.

PA (MARS/) MARSHALL J.

PA (YANT/) YANTHA J.

PA (VREE/) VREES T.

XX
 PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;

XX
 DR WPI; 2003-491923/46.

XX
 PT Determining proteomic basis e.g. basis for diagnosing existence of or

XX
 PT predicting development and/or progression of abnormal physiological

XX
 PT conditions based upon the presence of proteomic materials.

XX
 PS Disclosure; Page 10; 25pp; English.

CC The invention discloses a method for determining a proteomic basis for
 CC development and progression of abnormal physiological conditions. The
 CC method comprises isolating one or more patient specific proteomic
 CC materials from a sample and comparing it against a library of proteomic
 CC materials having characteristics identifiable with both normal and
 CC abnormal physiological conditions or their predictive hallmarks. The
 CC method is useful for determining a proteomic basis for development and
 CC progression of abnormal physiological conditions. The method is also
 CC useful for evaluating samples containing several analyte/biopolymers for
 CC the presence of physiological condition specific sequences. The peptide
 CC presented is a biomarker from alpha fibrinogen and is associated with
 CC renal failure

XX
 SQ Sequence 14 AA;

Query Match 54.0%; Score 27; DB 6; Length 14;
 Best Local Similarity 57.1%; Pred. No. 3.9e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPMIOGG 7
 ||: ||
 Db 4 DFLABCG 10

RESULT 28

AAR72938

ID	AA72938	standard; peptide; 9 AA.
XX		
AC	AA72938;	
XX		
DT	16-OCT-2003	(revised)
DT	25-MAR-2003	(revised)
DT	29-NOV-1995	(first entry)
XX		
DE	E. coli PPIase-beta cyanogen bromide cleavage fragment 2.	
XX		
KW	Escherichia coli; protein conformation; folding; acceleration;	
KW	PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;	
KW	isomerisation; prolyl peptide bond.	
XX		
OS	Escherichia coli; (ST 249 strain).	
XX		
PN	EP647714-A1.	
PD		
XX	12-APR-1995.	
XX		
PF	19-JUL-1990;	94EP-00203612.
XX		
PR	19-JUL-1989;	89JP-00184738.
PR	06-OCT-1989;	89UP-00260244.
PR	29-DEC-1989;	89JP-00344705.
PR	19-JUL-1990;	90EP-00307914.
PA		
XX	(TOFU) TONEN CORP.	
XX		
PI	Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;	
XX		
DR	WPI; 1995-140756/19.	
XX		
PT	New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate	
PT	the folding of proteins, partic. for activation of inactive recombinant	
PT	proteins.	
XX		
PS	Example 6; Page 27; 85pp; English.	
XX		
CC	AA72937-42 are cyanogen bromide cleavage fragments of E. coli PPIase-	
CC	beta (peptidyl prolyl cis trans isomerase). The E. coli PPIase-beta has a	
CC	single mol. wt. of about 20 kDa and a single isoelectric point of about	
CC	5.0. The enzyme catalyses the isomerisation of prolyl peptide bonds in	
CC	proteins and accelerates the folding of the protein. The inventors are	
CC	claiming a PPIase-beta. (Updated on 25-MAR-2003 to correct PN field.)	
CC	(Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to	
CC	correct PR field.) (Updated on 16-OCT-2003 to standardise OS field)	
XX		
SQ	Sequence 9 AA;	
Query Match	52.0%;	Score 26; DB 2; Length 9;
Best Local Similarity	83.3%;	Pred. No. 1.4e+06;
Matches	5; Conservative	0; Mismatches 1; Indels 0; Gaps 0.
DY	4 IQGGDF 9 1 IQGGGF 6	
Db		
RESULT 29		
ID	AA72894	
XX	AA72894 standard; peptide; 9 AA.	
AC	AA72894;	
XX		
DT	16-OCT-2003	(revised)
DT	25-MAR-2003	(revised)
DT	29-NOV-1995	(first entry)
XX		
DE	E. coli PPIase-beta cyanogen bromide cleavage fragment 2.	
XX		
KW	Escherichia coli; protein conformation; folding; acceleration;	
KW	PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;	

KW	isomerisation; prolyl peptide bond.
XX	
XX	Escherichia coli; (ST 249 strain).
OS	
XX	EP647713-A1.
PN	
PD	12-APR-1995.
XX	
PF	19-JUL-1990; 94EP-00203610.
XX	
XX	19-JUL-1989; 89JP-00184738.
FR	06-OCT-1989; 89JP-00260244.
PR	29-DEC-1989; 89JP-00344705.
XX	
XX	19-JUL-1990; 90EP-00307914.
PA	(TOFU) TONEN CORP.
PI	Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
XX	
DR	WP; 1995-140755/19.
XX	
PT	New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate
PR	the folding of proteins, partic. for activation of inactive recombinant
XX	proteins.
XX	
PS	Example 6; Page 27; 85pp; English.
XX	
CC	AA02893-98 are cyanogen bromide cleavage fragments of E. coli PPIase-
CC	beta (peptidyl prolyl cis trans isomerase). The E. coli PPIase-beta has a
CC	single mol. wt. of about 20 kDa and a single isoelectric point of about
CC	5.0. the enzyme catalyses the isomerisation of prolyl peptide bonds in
CC	proteins and accelerates the folding of the protein. The inventors are
CC	claiming the PPIase-alpha. (Updated on 25-MAR-2003 to correct PN field.)
CC	(Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to
CC	correct PR field.) (Updated on 16-OCT-2003 to standardise OS field)
XX	
SO	Sequence 9 AA;
QY	4 IQGGDF 9
DB	1 IQGGGF 6
Query Match	52.0%; Score 26; DB 2; Length 9;
Best Local Similarity	83.3%; Pred. No. 1.4e+06;
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
RESULT 30	
ID	AA02949 standard; peptide; 10 AA.
AC	AA02949;
XX	
DT	16-OCT-2003 (revised)
DT	25-MAR-2003 (revised)
DT	29-NOV-1995 (first entry)
XX	
XX	E. coli PPIase-alpha cyanogen bromide cleavage fragment 1.
XX	
KM	Escherichia coli; protein conformation; folding; acceleration;
KM	PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
KM	isomerisation; prolyl peptide bond.
XX	
OS	Escherichia coli; (ST 249 strain).
XX	
PN	EP647714-A1.
XX	
PD	12-APR-1995.
XX	
PF	19-JUL-1990; 94EP-00203612.
XX	
FR	19-JUL-1989; 89JP-00184738.
PR	06-OCT-1989; 89JP-00260244.

PR 29-DEC-1989; 89JP-00344705.
 PR 19-JUL-1990; 90EP-00307914.
 XX
 PA (TORU) TONEN CORP.
 XX
 PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
 XX WPI; 1995-140756/19.
 DR
 XX New E.coli peptidyl prolyl cis trans isomerase beta - used to accelerate
 PT the folding of proteins, partic. for activation of inactive recombinant
 PT proteins.
 XX
 PS Example 7; Page 30; 85pp; English.
 XX
 CC AAR72949-52 are cyanogen bromide cleavage fragments of E. coli PPIase-
 CC alpha (peptidyl prolyl cis trans isomerase). The E. coli PPIase-alpha has
 CC a single mol. wt. of about 22 kDa and a single isoelectric point of about
 CC 9.7. The enzyme catalyses the isomerisation of prolyl peptide bonds in
 CC proteins and accelerates the folding of the protein. The inventors are
 CC claiming a PPIase-beta. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 16-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 10 AA;
 XX
 Query Match 52.0%; Score 26; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 IQGGDF 9
 Db 1 IQGGGF 6
 XX
 RESULT 31
 AAR72905
 ID AAR72905 standard; peptide; 10 AA.
 XX
 AC AAR72905;
 XX
 DT 16-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 29-NOV-1995 (first entry)
 XX
 DE E. coli PPIase-alpha cyanogen bromide cleavage fragment 1.
 XX
 KW Escherichia coli; protein conformation; folding; acceleration;
 KW PPIase-alpha; peptidyl prolyl cis trans isomerase alpha; catalysis;
 KW isomerisation; prolyl peptide bond.
 XX
 OS Escherichia coli; (Str 249 strain).
 XX
 PN EP647713-A1.
 PD 12-APR-1995.
 XX
 PF 19-JUL-1990; 94EP-00203610.
 PF 19-JUL-1990;
 PR 19-JUL-1989; 88JP-00184738.
 PR 06-OCT-1989; 88JP-00280244.
 PR 29-DEC-1989; 89JP-00344705.
 PR 19-JUL-1990; 90EP-00307914.
 XX
 PA (TORU) TONEN CORP.
 XX
 PI Hayano T, Katou S, Maki N, Takahashi N, Suzuki M;
 XX WPI; 1995-140755/19.
 DR
 XX New E.coli peptidyl prolyl cis trans isomerase alpha - used to accelerate
 PT the folding of proteins, partic. for activation of inactive recombinant
 PT proteins.

XX
 PS Example 7; Page 30; 85pp; English.
 XX
 CC AAR72905-08 are cyanogen bromide cleavage fragments of E. coli PPIase-
 CC alpha (peptidyl prolyl cis trans isomerase). The E. coli PPIase-alpha has
 CC a single mol. wt. of about 22 kDa and a single isoelectric point of about
 CC 9.7. The enzyme catalyses the isomerisation of prolyl peptide bonds in
 CC proteins and accelerates the folding of the protein. The inventors are
 CC claiming the PPIase-alpha. (Updated on 25-MAR-2003 to correct PN field.)
 CC (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to
 CC correct PR field.) (Updated on 16-OCT-2003 to standardise OS field)
 CC
 SQ Sequence 10 AA;
 XX
 Query Match 52.0%; Score 26; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 4.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 IQGGDF 9
 Db 1 IQGGGF 6
 XX
 RESULT 32
 AAR21441
 ID AAR21441 standard; peptide; 12 AA.
 XX
 AC AAR21441;
 XX
 DT 29-JUL-1997 (first entry)
 XX
 DE HSV glycoprotein B derived signal oligopeptide #3.
 XX
 KW Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; STV;
 KW competitive inhibitor; feedback regulator; synthetis; gastrin precursor;
 KW charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
 KW hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
 KW gonadoliberin precursor; plasminogen activator inhibitor 2; protein;
 KW Alzheimer amyloid A4; corticotropin releasing factor binding protein;
 KW apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVVS;
 KW herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A1;
 KW Treponema pallidum membrane protein; TMAP; islet amyloid polypeptide;
 KW fibroblast MPPI; schistosoma elastase precursor; schistosomin;
 KW hepatitis delta antigen; rev protein; HIV; VILV; angiotensinogen.
 XX
 OS Herpes simplex virus.
 XX
 PN WO9519568-A1.
 PD 20-JUL-1995.
 XX
 PF 12-JAN-1995; 95WO-US000575.
 PR 14-JAN-1994; 94US-00182248.
 XX
 PA (RATH/) RATH M.
 PI Rath M;
 XX
 DR WPI; 1995-263953/34.
 PT Identifying signal oligopeptide(s) in protein sequence(s) - shown as
 PT regions of max. hydrophilicity, used in modulating communication between
 PT protein(s).
 XX
 PS Claim 5; Page 63; 88pp; English.
 XX
 CC The sequences given in AAR21201-560 represent hydrophilic signal oligo-
 CC peptides. These signal oligopeptides are localised on the surface of the
 CC protein and are represented by the hydrophilicity maxima of the protein.
 CC These peptides are enriched in charged amino acids arranged with neutral
 CC spacer amino acids. The specific signal character of these oligopeptides
 CC is determined by a characteristic combination of conformation and charge

CC within the signal sequence. These oligopeptides may be used as vaccines
CC in the treatment of human disease, as competitive inhibitors to prevent
CC or reduce the metabolic action or interaction of a selected protein by
CC blocking its specific signal sequences, or as therapeutic agents to
CC function as feedback regulators to reduce synthesis rate of a selected
CC protein. These peptides may be modified by omitting one or more amino
CC acids at the N- and/or C-terminal, by substituting one or more amino
CC acids without consideration of charge and polarity, by substituting one
CC or more amino acids with amino acid residues with similar charge and/or
CC polarity, by omitting one or more amino acids or a combination of these
CC

SQ Sequence 12 AA;

Query Match 52.0%; Score 26; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 OGGDF 9
|:|:|:
Db 4 BGGDF 8

RESULT 33

ID AAB44921 standard; protein; 12 AA.

AC AAB44921;

DT 12-FEB-2001 (first entry)

XX Human secreted protein encoded by gene 5.

KM Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;
KM antiproliferative; cytostatic; cardiatic; vasotropic; cerebroprotective;
KM neurotropic; neuroprotective; antibacterial; virucide; fungicide;
KM ophthalmological; gene therapy; treatment; autoimmune disease; infection;
KM cardiovascular disorder; nervous system disorder; ocular disorder;
KM wound healing; epithelial cell proliferation; skin aging; mental state;
KM transplantation; metabolism modulation.

XX Homo sapiens.

PN WO200055200-A1.

XX 21-SEP-2000.

PF 09-MAR-2000; 2000WO-US006042.

PR 12-MAR-1999; 99US-0124143P.

PR 03-DEC-1999; 99US-0168663P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsoulis G;

DR WPI; 2000-656008/63.

DR N-PSDB; AAC79902.

PT Isolated human secretory proteins, nucleic acids encoding them and
PT antibodies directed against them, useful for diagnosing and treating
PT disorders related to the proteins such as cancer, Alzheimer's disease and
PT Parkinsons.

PS Claim 11; Page 382; 453p; English.

XX This invention describes a novel isolated polypeptide (I) and its
XX encoding nucleic acid molecule (II) which have immunosuppressive,
XX antirheumatic, antirheumatic, antiproliferative, cytostatic, cardiatic,
XX vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,
XX virucide, fungicide and ophthalmological activity and which can be used
XX for gene therapy. (I) and (II) are used to prevent, treat or ameliorate a
XX medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
XX dogs, chickens or sheep. (I) and (II) are also used in diagnosing a

CC pathological condition or susceptibility to a pathological condition. The
CC antibodies to (II) can also be used in alleviating symptoms associated
CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays
CC or enzyme linked immunosorbent assays (ELISA). Disorders which are
CC diagnosed or treated include autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiodysgenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides are used to
CC modulate mammalian metabolism, to change mammal's mental state or
CC physical state by influencing biorhythms circadian rhythms, depression
CC tendency for violence tolerance for pain, reproductive capabilities,
CC hormonal or endocrine levels, appetite, libido, memory, stress or other
CC cognitive qualities, as a food additive or preservative, such as to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrates, vitamins, minerals, cofactors or other nutritional
CC components

SQ Sequence 12 AA;

Query Match 52.0%; Score 26; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 FMTGGDF 9
|:|:|:
Db 3 FSIKGDF 10

RESULT 34

ID AAB68410 standard; peptide; 14 AA.

AC AAB68410;

DT 16-JAN-2002 (first entry)

DX Human Breast cancer-associated protein isoform, BPI-244 peptide #1.

DX Human Breast cancer-associated protein isoform; breast cancer;

DX Human; Breast cancer-associated protein isoform; breast cancer;

DX Homo sapiens.

PN WO200171357-A2.

XX 27-SEP-2001.

PF 20-MAR-2001; 2001WO-GB001219.

PR 20-MAR-2000; 2000GB-00006695.

PR 24-MAR-2000; 2000GB-00007265.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMAc, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

DR WPI; 2001-611532/70.

XX Identifying proteins for clinical screening, diagnosis and prognosis of
XX breast cancer, comprises detecting Breast Cancer-Associated Protein
XX Isoforms (BPIs) using two-dimensional electrophoresis.

PS Claim 9; Page 51; 197p; English.

XX The invention relates to diagnosing, determining the stage or severity,
XX or identifying the risk of a subject developing cancer (especially breast
XX cancer), or monitoring the effect of therapy on a subject with cancer.

CC comprising analysing a test sample using two-dimensional electrophoresis
 CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
 CC methods disclosed are used for the diagnosis and prognosis of breast
 CC cancer, for determining the severity of breast cancer, and for
 CC identifying a subject at risk of developing breast cancer, and monitoring
 CC the effect of therapy administered to a subject. Antibodies raised
 CC against the binding domain of a BPI, the binding domain of a BPI, a
 CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
 CC of a BPI can be incorporated into a pharmaceutical composition for
 CC treating or preventing breast cancer. The methods use sensitive and
 CC specific biomarkers provide early diagnosis of breast cancer, and the
 CC compositions are more potent, specific, and has a more rapid effect with
 CC fewer side effects than other prior art methods. The present sequence is
 CC a tryptic digest peptide from a BPI of the invention

Sequence 14 AA:

Query Match 52.0%; Score 26; DB 4; Length 14;
 Best Local Similarity 44.4%; Pred. No. 5.9e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPMIQQGDF 9
 1 DSLILQDGEF 9

RESULT 35
 AAU68401
 ID AAU68401 standard; peptide; 14 AA.
 AC AAU68401;

DT 16-JAN-2002 (first entry)

DE Human Breast cancer-associated protein isoform, BPI-357 peptide.

KM Human; Breast cancer-associated protein isoform; breast cancer;
 immunogen; cytosolic; BPI; tryptic digest peptide.

OS Homo sapiens.

PN WO200171357-A2.

PD 27-SEP-2001.

PF 20-MAR-2001; 2001WO-GB001219.

PR 20-MAR-2000; 2000GB-00006695.

PR 24-MAR-2000; 2000GB-00007265.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Herath HMC, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;

DR WPI; 2001-611532/70.

PT Identifying proteins for clinical screening, diagnosis and prognosis of
 breast cancer, comprises detecting Breast Cancer-Associated Protein
 isoforms (BPIs) using two-dimensional electrophoresis.

PS Claim 9; Page 51; 197pp; English.

CC The invention relates to diagnosing, determining the stage or severity,
 CC or identifying the risk of a subject developing cancer (especially breast
 CC cancer), or monitoring the effect of therapy on a subject with cancer,
 CC comprising analysing a test sample using two-dimensional electrophoresis
 CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
 CC methods disclosed are used for the diagnosis and prognosis of breast
 CC cancer, for determining the severity of breast cancer, and for
 CC identifying a subject at risk of developing breast cancer, and monitoring
 CC the effect of therapy administered to a subject. Antibodies raised
 CC against the binding domain of a BPI, the binding domain of a BPI, a
 CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function

CC of a BPI can be incorporated into a pharmaceutical composition for
 CC treating or preventing breast cancer. The methods use sensitive and
 CC specific biomarkers provide early diagnosis of breast cancer, and the
 CC compositions are more potent, specific, and has a more rapid effect with
 CC fewer side effects than other prior art methods. The present sequence is
 CC a tryptic digest peptide from a BPI of the invention

Sequence 14 AA:

Query Match 52.0%; Score 26; DB 4; Length 14;
 Best Local Similarity 44.4%; Pred. No. 5.9e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPMIQQGDF 9
 1 DSLILQDGEF 9

RESULT 36
 ABR75514
 ID ABR75514 standard; peptide; 14 AA.
 AC ABR75514;

DT 28-AUG-2003 (first entry)

DE Liver response-associated protein isoform (LRPI) peptide SEQ ID NO.75.

KM Biomarker; liver response; liver response-associated protein isoform;
 LRPI; liver response-associated feature; LRP.

OS Synthetic.

PN WO2003038444-A2.

PD 08-MAY-2003.

PF 31-OCT-2002; 2002WO-US034847.

PR 31-OCT-2001; 2001US-0335964P.

PA (PFIZ) PFIZER PROD INC.
 (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PI Amacher DE, Fasulo LM, Herath HMC, Holt GD, Striger TR;

DR WPI; 2003-430566/40.

PT Screening, diagnosing, staging or identifying subject at risk of
 developing, liver response, or monitoring effect of therapy on liver
 response, by detecting Liver Response-Associated Protein Isoforms in
 subject sample.

PS Claim 1; Page 57; 256pp; English.

CC The present invention describes a method (M1) for screening or diagnosing
 CC a liver response in a subject, determining the stage or severity of a
 CC liver response in a subject, identifying a subject at risk of developing
 CC liver response, or monitoring the effect of therapy administered to a
 CC subject having liver response, involving detecting liver response-
 CC associated protein isoforms (LRPIs) (see the peptides given in ABR75395
 CC to ABR75806) in a test biological sample from the subject. Alternatively,
 CC screening or diagnosing a liver response in a subject, or monitoring the
 CC effect of a drug or therapy administered to a subject, involves
 CC contacting at least one oligonucleotide probe comprising 10 or more
 CC consecutive nucleotides complementary to a nucleotide sequence encoding
 CC an LRP1 with RNA obtained from a biological sample from the subject or
 CC with cDNA copied from the RNA, where the contacting occurs under
 CC conditions that permit hybridisation of the probe to the nucleotide
 CC sequence if present, detecting hybridisation, if any, between the probe
 CC and the nucleotide sequence, and comparing the hybridisation, if any,
 CC detected in the above step, with the hybridisation detected in a control
 CC sample, or with a previously determined reference range. M1 is useful for

CC screening or diagnosing a liver response in a subject, determining the
CC stage or severity of a liver response in a subject, identifying a subject
CC at risk of developing liver response, and monitoring the effect of
CC therapy administered to a subject having liver response
XX
SQ Sequence 14 AA;

Query Match 52.0%; Score 26; DB 6; Length 14;
Best Local Similarity 44.4%; Pred. No. 5.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFMIOGDP 9
| : : | : |
Db 1 DSLUDGEP 9

RESULT 37
AAR20729 standard; peptide; 9 AA.

AC AAR20729;
XX
DT 25-MAR-2003 (revised)
DT 12-MAY-1992 (first entry)
XX
DE Pancreas-elastase-1 antigenic peptide.
XX
KM E1; monoclonal antibody; immunoassay; epitope.
XX
OS Synthetic.

XX DE4107765-A.
XX 30-JAN-1992.
XX 11-MAR-1991; 91DE-04107765.
XX 28-JUL-1990; 90DE-04023972.
XX (SCHB-) SCHEBO TECH MBD-BIO.
XX
PI Szigoleit A, Scheefers H, Scheefers BU;
XX
DR WPI; 1992-042541/06.
XX
PT Obtaining pancreas-elastase-1-specific antibodies - using specific
PT peptide, for diagnosis of acute and chronic pancreatitis and
PT mucoviscidosis.
XX
PS Disclosure, Page 5; SPP; German.

XX The amino acid sequence is that of an antigenic peptide of pancreas
CC elastase-1 (E1) which is used to raise antibodies to E1. The antibodies
CC are used in immunoassay kits for qualitative and quantitative analysis of
CC E1 for diagnosis and monitoring of chronic and acute pancreatitis, and
CC mucoviscidosis in body fluids or faeces. (Updated on 25-MAR-2003 to
CC correct PI field.)
XX
SQ Sequence 9 AA;

Query Match 50.0%; Score 25; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGSD 8
| : : | : |
Db 2 MVAGSD 7

RESULT 38
AAV51905
ID AAV51905 standard; peptide; 9 AA.
XX

AC AAV51905;
XX
DT 15-JUN-2000 (first entry)
XX
DE Elastase immunogenic peptide.
XX
KM Immunogenic; pancreatic elastase; diagnosis; detection; isoenzyme;
KM pancreas; pancreatitis; cystic fibrosis.
XX
OS Unidentified.

XX DE19923892-A1.
XX 09-MAR-2000.
XX 25-MAY-1999; 99DE-01023892.
XX
PR 08-SEP-1998; 98DE-01040900.
XX
PA (PRIV-) PRIVATES INST BIOSERV GMBH.
XX
PI Heinrich H, Kleinert R, Meyer U, Wagner H;
XX
DR WPI; 2000-258170/23.

XX
PT Diagnosing disorders of pancreatic function such as pancreatitis, by
PT determining content of all pancreatic elastase isoenzymes in serum or
PT feces.
XX
PS Claim 2; Col 6; 6pp; German.

XX This invention describes a novel diagnostic method for detecting a
CC disorder of pancreatic function which comprises determining the total
CC content of all pancreatic elastases (isoenzymes) in serum, secretions or
CC excretions. The method can be used to diagnose or monitor pancreatic
CC disease such as chronic or acute pancreatitis. Test kits for detecting
CC elastase-1 can also be used for diagnosis and monitoring of cystic
CC fibrosis. The method is more sensitive than prior art tests that
CC determine only elastase-1. Antibodies raised against immunogenic
CC fragments of the different elastase isoforms are very specific and do not
CC react with other components of feces. AAV51858-151872 represent
CC pancreatic elastase immunogenic peptides described in the method of the
CC invention
XX

SQ Sequence 9 AA;
Query Match 50.0%; Score 25; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 MIOGSD 8
| : : | : |
Db 2 MVAGSD 7

RESULT 39
AAM22987
ID AAM22987 standard; peptide; 9 AA.

XX AAM22987;
XX
DT 22-OCT-2001 (first entry)
XX
DE HIV peptide SEQ ID NO 872.
XX
KM Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
KM human immunodeficiency virus; vaccine.
XX
OS Human immunodeficiency virus.
OS Synthetic.
XX
PN WO200155177-A2.
XX

PD 02-AUG-2001.
 XX
 PF 29-JAN-2001; 2001WO-DK000059.
 XX
 PR 28-JAN-2000; 2000EP-00610017.
 PR 31-JAN-2000; 2000US-0179333P.
 XX
 PA (STAT-) STATENS SERUM INST.
 XX
 PI Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J,
 XX
 DR WPI; 2001-476184/51.
 XX
 PT The generation of cytotoxic T cell lymphocytes epitopes for use in anti-
 PT HIV vaccines.
 XX
 PS Example 4; Page 70; 383pp; English.
 XX
 CC The invention relates to identification of cytotoxic T cell lymphocyte
 CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
 CC are a major protective mechanism against viral diseases. Antibodies may
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
 CC prevent infection of cells in the host, but CTL will limit viral
 CC production by killing the cell. The CTL epitopes are useful in medicine,
 CC in the manufacture of vaccines or diagnostic agents
 CC
 SQ Sequence 9 AA;
 Query Match Score 25; DB 4; Length 9;
 Best Local Similarity 71.4%; Pred. No. 14e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 MIQGDGF 9
 Db 1 MIQGNF 7
 RESULT 40
 ID AAV78392 standard; peptide; 10 AA.
 AC AAV78392;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Biosurfactant peptide #11.
 XX
 KW Biosurfactant; antibacterial; vulnerary; anti-pathogenic; antifungal;
 KW antiviral; protozoacide; collagen receptor; Staphylococcus aureus;
 KW methicillin resistant; Pseudomonas aeruginosa; Enterococcus faecalis;
 KW vancomycin resistant; Bacteroides; infection; heart valve; joint;
 KW artificial vein; stent; prosthetic; intravenous line; catheter;
 KW diaphragm; tampon; wound; biofilm.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8 /label= Ser, His
 FT Misc-difference 9 /label= Ser, His
 FT
 WO200212271-A2.
 PN
 PD 14-FEB-2002.
 XX
 PF 03-AUG-2001; 2001WO-IB001717.
 PF
 PR 04-AUG-2000; 2000US-0223065P.
 PR
 PA (HOWA/) HOWARD J.
 PA (REID/) REID G.
 PA (GANB/) GAN B S.

XX
 PI Howard J, Reid G, Gan BS;
 XX
 DR WPI; 2002-280689/32.
 XX
 PT New isolated biosurfactant peptides useful for treating pathogenic
 PT bacterial infections in a subject.
 XX
 PS Example 4; Page 35; 42pp; English.
 XX
 CC The invention relates to a novel isolated biosurfactant peptide. The
 CC peptides are used for inhibiting the binding of a pathogen to a collagen
 CC receptor and treating an infection in a subject, caused by e.g.
 CC Staphylococcus aureus (e.g. methicillin-resistant - MRSA), S. epidermidis
 CC (e.g. methicillin-resistant - MRSE), Pseudomonas aeruginosa, Enterococcus
 CC faecalis (e.g. vancomycin-resistant - VRE), Bacteroides sp., and also
 CC fungal, viral and protozoal infections. The peptides are useful for
 CC coating implanted surgical devices such as heart valves, artificial
 CC veins, joints, stents, tubes, prosthetics, bandages, intravenous lines,
 CC catheters, diaphragms and tampons; and are also useful in compositions to
 CC combat infectious complication rates associated with the use of surgical
 CC implant sites; and for the treatment of infections occurring at wound
 CC sites. The peptides inhibit infections around wounds and at the site of
 CC implants and biofilms, which are associated with infections in mammals,
 CC in vivo. The peptides are derived from human microorganism isolates and
 CC hence are non-immunogenic, non-pathogenic, non-carcinogenic, and non-
 CC invasive when administered to humans. The biosurfactant peptide can act
 CC as a signaling molecule which can turn off a pathogen's virulence
 CC capability. The present sequence represents a biosurfactant peptide of
 CC the invention
 CC
 SQ Sequence 10 AA;
 Query Match Score 25; DB 5; Length 10;
 Best Local Similarity 80.0%; Pred. No. 6.1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 IQGSD 8
 Db 2 IQGSD 6
 RESULT 41
 ID AAG98171 standard; peptide; 14 AA.
 AC AAG98171;
 XX
 DT 19-SEP-2001 (first entry)
 XX
 DE Human SNP associated peptide SEQ ID NO. 813.
 XX
 KW Human; single nucleotide polymorphism; SNP; angiotensin;
 KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
 KW adenosine triphosphate-dependent RNA helicase;
 KW major histocompatibility complex Class I histocompatibility antigen; MHC;
 KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
 KW antileukemic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
 KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200148245-A2.
 PD
 PD 05-JUL-2001.
 XX
 PF 27-DEC-2000; 2000WO-US035346.
 PF
 PR 27-DEC-1999; 99US-00472688.
 PR
 PA (CURA-) CURAGEN CORP.
 PA
 XX Shinketsu RA, Leach M;
 PI

XX WPI; 2001-418297/44.
 DR
 XX Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
 PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
 PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
 PT diseases and infections.
 XX
 PS Disclosure; Page 469; 484pp; English.
 XX
 CC The invention relates to nucleic acids (AAH9386-AAH90036) encoding
 CC polymorphic variants of proteins (AA998010-AA998238) related to
 CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
 CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
 CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
 CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
 CC proteins have potential immunosuppressive, immunostimulatory,
 CC antineoplastic, antidiabetic, antihypertensive, antiinflammatory, cytostatic,
 CC antileukemic, neuroprotective and antimicrobial activity and may be
 CC useful in gene/protein therapy, vaccines, modulation of the expression
 CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
 CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major
 CC histocompatibility complex (MHC) Class I histocompatibility antigen
 CC and/or phosphoglycerate kinase. Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include multifactorial
 CC diseases with a genetic component, such as autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
 CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of
 CC the bladder, brain, breast, colon and kidney, leukemia), diseases of the
 CC nervous system, an infection of pathogenic organisms. They may also be
 CC used to alter phenotypic traits such as longevity, appearance, strength,
 CC speed and endurance
 XX
 SQ Sequence 14 AA;
 XX
 Query Match 50.0%; Score 25; DB 4; Length 14;
 Best Local Similarity 55.6%; Pred. No. 8.8e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DFMIOGGDF 9
 Db 3 DEYMGGFF 11
 XX
 RESULT 42
 AA09052
 ID AA09052 standard; peptide; 8 AA.
 XX
 AC AA09052;
 XX
 DT 06-JUL-1999 (first entry)
 XX
 DE Synthetic peptide used in tests for BSP-binding inhibition.
 XX
 KM Bone sialoprotein; BSP; inhibits staphylococcal bacterial adhesion;
 KM osteomyelitis; septic arthritis; antibiotic resistance; fusion.
 XX
 OS Synthetic.
 XX
 PN WO916792-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 23-SEP-1998; 98WO-SE001708.
 XX
 PR 25-SEP-1997; 97SF-00005614.
 XX
 PA (RYDE/) RYDEN C.
 PA (OLDB/) OLDBERG A.
 XX
 PI Ryden C, Oldberg A;
 XX
 DR WPI; 1999-263687/22.

XX Bone sialoprotein (BSP) derived polypeptides inhibit binding between BSP
 PT and staphylococcal cells.
 XX
 PS Disclosure; Page 28; 33pp; English.
 XX
 CC The invention relates to a bone sialoprotein (BSP)-derived protein that
 CC has ability to inhibit the binding of BSP to staphylococcal cells. The
 CC BSP-derived polypeptide has the ability to bind to staphylococcal cells
 CC and can be used to inhibit staphylococcal adhesion to tissues or
 CC implants. In particular it is useful for inhibiting osteomyelitis and/or
 CC septic arthritis. The BSP-derived peptides can be used as alternatives to
 CC antibiotics thereby not adding to an increase in staphylococcal
 CC antibiotic resistance
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 48.0%; Score 24; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 FMIQGG 7
 Db 3 FPIVQGG 8
 XX
 RESULT 43
 AAB12089
 ID AAB12089 standard; peptide; 8 AA.
 XX
 AC AAB12089;
 XX
 DT 12-SEP-2003 (revised)
 DT 17-JAN-2001 (first entry)
 XX
 DE Ad7 cell peptide.
 XX
 KM Rb-interacting zinc finger; RIZ; retinoblastoma; heart disease;
 KM cell proliferation; cell differentiation; tissue repair;
 KM transcription regulator; breast cancer; gene therapy; melanoma;
 KM neuroblastoma; leukemia; Parkinson's disease; Huntington's disease;
 KM Alzheimer's disease; paralysis; motor neuron disorder; cell.
 XX
 OS unidentified adenovirus.
 XX
 PN US6069231-A.
 XX
 PD 30-MAY-2000.
 XX
 PF 18-AUG-1995; 95US-00516859.
 XX
 PR 18-AUG-1994; 94US-00292683.
 PR 06-MAR-1995; 95US-00399411.
 XX
 PA (LJOL-) LA JOLLA CANCER RES FOUND.
 XX
 PI Huang S;
 XX
 DR WPI; 2000-410879/35.
 XX
 PT New PR domain peptides comprising amino acid sequences from, for example
 PT retinoblastoma-interacting zinc finger, or egl-43 proteins, for
 PT regulating gene transcription and controlling cell proliferation and
 PT differentiation.
 XX
 PS Disclosure; Fig 2; 91pp; English.
 XX
 CC The present sequence is Ad7 cell from Adenovirus. The cell domain is also
 CC found in rat retinoblastoma (Rb)-interacting zinc finger (RIZ) protein
 CC (AAB12028). RIZ is a nuclear phosphoprotein that acts as a cell
 CC differentiation factor. RIZ can modulate cell growth by binding to Rb
 CC protein, which is involved in regulating cell proliferation. In addition,
 CC RIZ can act to regulate transcription. RIZ functions to maintain cells in

CC the G1 phase of the cell cycle, by interacting with Rb through the cR2
 CC domain of RIZ. Rat RIZ protein contains a number of GTPase motifs (see
 CC AAB12037 to AAB12056 and AAB12099 to AAB12104). RIZ protein is a PR
 CC domain protein and is present primarily in the cell nucleus. RIZ gene
 CC mutations may be implicated in various cancers such as melanoma.
 CC neuroblastoma, leukemia and breast cancer, and so the RIZ gene may be
 CC used in gene therapy for these disorders. Since RIZ protein is implicated
 CC in cell cycle arrest, inhibition of RIZ activity may be useful in
 CC neurodegenerative disorder therapy e.g. for Parkinson's, Huntington's or
 CC Alzheimer's disease, paralysis or motor neurone disorders, or cardiac
 CC disorders e.g. heart disease, where the ability to induce neural/cardiacc
 CC tissue proliferation would be useful. The present sequence was used for
 CC sequence homology comparison. (Updated on 12-SEP-2003 to standardise OS
 CC field)

CC Sequence 8 AA;

Query Match 48.0%; Score 24; DB 3; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOGGD 8
 Db 3 LIEGGD 8

RESULT 44
 ADE84662

ID ADE84662 standard; peptide; 8 AA.

AC ADE84662;

DT 29-JAN-2004 (first entry)

DE Adenovirus 7 E1A gene cel domain.

KM cytostatic; tumor; gene therapy;
 KM retinoblastoma protein-interacting zinc protein; RIZ; neuroblastoma;
 KM melanoma; cardiac cell growth inducer; neuronal cell growth inducer;
 KM adenovirus; E1A; cel.

OS unidentified adenovirus.

PN US6468985-B1.

PD 22-OCT-2002.

PF 17-MAR-2000; 2000US-00528706.

PR 18-AUG-1994; 94US-00282683.

PR 06-MAR-1995; 95US-00399411.

PR 18-AUG-1995; 95US-00516859.

PA (BURN-) BURNHAM INST.

PI Huang S;

DR WPI; 2003-147106/14.

PT Reducing the growth of tumor cell having mammalian retinoblastoma protein

PT -interacting zinc finger proteins in a subject, comprises administering

PT nucleic acid molecule encoding RIZ at or adjacent to the site of tumor.

PS Example 3; SEQ ID NO 75; 49pp; English.

CC The invention describes a method of reducing growth of a tumour cell
 CC having a mutant mammalian retinoblastoma (Rb) protein-interacting zinc
 CC finger (RIZ) protein in a subject. The method comprises administering a
 CC nucleic acid molecule (I) encoding RIZ at or adjacent to tumour site. (1)
 CC is administered at the site of the tumour. The method is useful for
 CC reducing the growth of a tumour cell e.g. neuroblastoma or melanoma cell
 CC having mutant RIZ protein. The method is useful for inducing growth of a
 CC cardiac cell or a neuronal cell in a subject, and for effecting normal

CC growth control to a tumour cell or causing differentiation of tumour
 CC cells. This is the amino acid sequence of an adenovirus cxi domain used
 CC in a comparison with the cel domain of RIZ protein.

CC Sequence 8 AA;

Query Match 48.0%; Score 24; DB 7; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+06;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MIOGGD 8
 Db 3 LIEGGD 8

RESULT 45

ID AAY09051 standard; peptide; 9 AA.

AC AAY09051;

DT 06-JUL-1999 (first entry)

DE BSP-binding inhibiting synthetic peptide.

KM Bone sialoprotein; BSP; inhibit; staphylococcal; bacterial adhesion;
 KM osteomyelitis; septic arthritis; antibiotic resistance; fusion.

OS Synthetic.

PN WO9916792-A1.

PD 08-APR-1999.

PF 23-SEP-1998; 98WO-SER01708.

PR 25-SEP-1997; 97SE-00003614.

PA (RYDEN/) RYDEN C.

PA (OLDB/) OLDBERG A.

PI Ryden C, Oldberg A;

DR WPI; 1999-263687/22.

PT Bone sialoprotein (BSP) derived polypeptides inhibit binding between BSP

PT and staphylococcal cells.

PS Claim 6; Page 28; 33pp; English.

CC The invention relates to a bone sialoprotein (BSP)-derived protein that
 CC has ability to inhibit the binding of BSP to staphylococcal cells. The
 CC BSP-derived polypeptide has the ability to bind to staphylococcal cells
 CC and can be used to inhibit staphylococcal adhesion to tissues or
 CC implants. In particular it is useful for inhibiting osteomyelitis and/or
 CC septic arthritis. The BSP-derived peptides can be used as alternatives to
 CC antibiotics thereby not adding to an increase in staphylococcal
 CC antibiotic resistance. The present sequence represents a synthetic
 CC peptide that can inhibit BSP-binding to staphylococcal cells

CC Sequence 9 AA;

Query Match 48.0%; Score 24; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.4e+06;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FMIOGG 7
 Db 4 FVIOGG 9

Search completed: August 30, 2004, 10:49:24
 Job time: 17.4088 secs

Thu Sep 2 07:41:31 2004

us-09-720-469a-2.aug30.rag

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:34 ; Search time 8.66554 Seconds
(without alignments)
327.696 Million cell updates/sec

Title: US-09-720-469A-3

Perfect score: 51

Sequence: 1 GFGYKNSKF 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 3347

Minimum DB seq length: 8

Maximum DB seq length: 14

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	43.1	13	6	Q865C9 sus scrofa
2	20	39.2	12	4	Q866B2 homo sapien
3	18	35.3	9	2	P83529 lactobacilli
4	18	35.3	10	2	Q52837 rhizodum 1
5	18	35.3	13	13	P82866 rana pipien
6	18	35.3	14	6	Q9TRQ7 bos taurus
7	18	35.3	14	10	Q822V1 zea mays (m
8	18	35.3	14	12	Q86922 human cytom
9	18	35.3	14	12	Q85718 reovirus (t
10	18	35.3	14	13	P70007 xenopus lae
11	17	33.3	9	11	Q86G13 mus musculu
12	17	33.3	10	2	Q9X533 escherichia
13	17	33.3	10	2	Q9X534 leclercia a
14	17	33.3	10	8	Q8HUB4 anomobryum
15	17	33.3	11	2	Q47059 escherichia
16	17	33.3	11	5	Q9N165 ascaris suu

17	17	33.3	11	10	Q941R5	Q941R5 pinus radia
18	17	33.3	12	6	Q9TTE3	Q9TTE3 sus scrofa
19	17	33.3	12	8	Q8HUB3	Q8HUB3 bryum donia
20	17	33.3	13	2	Q47601	Q47601 escherichia
21	17	33.3	13	11	P82808	P82808 rattus norv
22	16	31.4	8	2	Q7X4C1	Q7X4C1 potato wirc
23	16	31.4	9	4	Q9B1F9	Q9B1F9 homo sapien
24	16	31.4	10	2	Q54217	Q54217 staphylococ
25	16	31.4	10	12	Q86580	Q86580 simian para
26	16	31.4	11	3	Q9UR95	Q9UR95 pichia angu
27	16	31.4	11	12	Q86916	Q86916 avian infec
28	16	31.4	12	10	Q9S8F0	Q9S8F0 zea mays (m
29	16	31.4	13	5	Q9U5J3	Q9U5J3 trypanosoma
30	16	31.4	13	5	Q9NC73	Q9NC73 oxytricha t
31	16	31.4	13	7	Q29823	Q29823 homo sapien
32	16	31.4	13	10	Q7X9Y2	Q7X9Y2 lycopersico
33	16	31.4	14	2	Q8KSE3	Q8KSE3 enterococcu
34	16	31.4	14	10	Q941T6	Q941T6 fragaria nu
35	16	31.4	14	10	Q945F2	Q945F2 cicor ariet
36	15	29.4	8	4	Q9U5F0	Q9U5F0 homo sapien
37	15	29.4	10	2	Q8BDC0	Q8BDC0 escherichia
38	15	29.4	10	4	Q9UN90	Q9UN90 homo sapien
39	15	29.4	10	5	Q26093	Q26093 plasaster oc
40	15	29.4	11	5	Q25916	Q25916 plasmodium
41	15	29.4	11	8	Q9GH12	Q9GH12 pandorina t
42	15	29.4	11	8	Q32704	Q32704 nicotiana t
43	15	29.4	11	11	Q9QVH3	Q9QVH3 rattus sp.
44	15	29.4	12	2	Q8KH47	Q8KH47 enterococcu
45	15	29.4	12	2	Q53579	Q53579 rhodobacter

ALIGNMENTS

RESULT 1	Q865C9	PRELIMINARY;	PRT;	13 AA.
ID	Q865C9			
AC	Q865C9			
DT	01-JUN-2003 (TREMURel. 24, Created)			
DT	01-JUN-2003 (TREMURel. 24, Last sequence update)			
DT	01-JUN-2003 (TREMURel. 24, Last annotation update)			
DE	Glutamine synthetase (Fragment).			
OS	Sus scrofa (Pig).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.			
OX	NCBI_TaxID=9623;			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RA	Kim J.G., Vallet J.L., Christenson R.K.;			
RT	"Characterization of porcine glutamine synthetase."			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AY216477; AAC64254.1; -			
FT	NON TER			
FT	SEQUENCE 13 AA; 1555 MW; 87987A0B71AB6B1A CRC64;			
Query Match	43.1%;	Score 22;	DB 6;	Length 13;
Best Local Similarity	80.0%;	Pred. No. 3e+03;		
Matches	4;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
QY	2 FGYN 6			
Db	9 FGYN 13			
RESULT 2	Q8N6B2	PRELIMINARY;	PRT;	12 AA.
ID	Q8N6B2			
AC	Q8N6B2			
DT	01-OCT-2002 (TREMURel. 22, Created)			
DT	01-OCT-2002 (TREMURel. 22, Last sequence update)			
DT	01-OCT-2002 (TREMURel. 22, Last annotation update)			
DE	Capacitative calcium channel protein Trp1 (Fragment).			
OS	Homo sapiens (Human).			

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=late pregnancy myometrium;
 RX MEDLINE=22181008; PubMed=12193412;
 RA Yang M., Gupta A., Shlykov S.G., Corrigan B., Tsujimoto S.,
 RA Sandorn B.M.,
 RT "Multiple Trp isoforms implicated in capacitative calcium entry are
 RT expressed in human pregnant myometrium and myometrial cells.";
 RL Biol. Reprod. 67:988-994(2002).
 DR EMBL: AF483645; AAM97860.1; --
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1511 MW; 4BF47B69BFB5053 CRC64;

Query Match 39.2%; Score 20; DB 4; Length 12;
 Best Local Similarity 75.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYXN 6
 |||
 Db 1 GYEN 4

RESULT 3
 P83529 PRELIMINARY; PRT; 9 AA.
 AC P83529;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DE Unknown protein from 2D-page (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 OX NCBI_TaxID=1625;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 20451;
 RX PubMed=12112860;
 RA Drews O., Weiss W., Reil G., Parlar H., Walt R., Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 RT Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774(2002).
 CC -1- MICELIAROUS: ON THE 2D-GEL THE DETERMINED MW OF THIS UNKNOWN
 CC PROTEIN IS: 15 KDA.
 CC FT NON_TER 1 9
 FT NON_TER 1 9
 SQ SEQUENCE 9 AA; 988 MW; 1031B1B1A729C86B CRC64;

Query Match 35.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1e+06;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPGY 4
 |||
 Db 1 GYGF 4

RESULT 4
 Q52837 PRELIMINARY; PRT; 10 AA.
 ID Q52837;
 AC Q52837;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Fixx protein (10 AA) (Fragment).
 OS Rhizobium leguminosarum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 OX NCBI_TaxID=384;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=PRE;
 RX MEDLINE=90136072; PubMed=2693897;
 RA Roelvyuk P.W., Hontelez J.G.J., Van Kammen A., van den Bos R.C.;
 RT "Nucleotide sequence of the regulatory nifA gene of Rhizobium
 RT leguminosarum PRE: transcriptional control sites and expression in
 RT Escherichia coli.";
 RL Mol. Microbiol. 3:1441-1447(1989).
 DR EMBL: X17073; CAA34923.1; --
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA; 1037 MW; 2A559372C879C9 CRC64;

Query Match 35.3%; Score 18; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
 |||
 Db 3 GFG 5

RESULT 5
 P82866 PRELIMINARY; PRT; 13 AA.
 AC P82866;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE RNA-binding protein (Fragment).
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Embryonic epithelium;
 RA Banerjee H.N., Blackmon R.H., Moses A., Harmon G.L., Peterson B.L.,
 RA Khan A.;
 RT "Isolation, identification and characterization of a novel 5'UTR
 RT binding protein for VCAM-1.";
 RL Submitted (NOV-2000) to Swiss-Prot.
 CC -1- FUNCTION: BINDS TO THE VCAM-1 5'UTR REGION.
 CC -1- SIMILARITY: TO THE FETUIN FAMILY.
 CC PIR: A59387; A59387.
 DR GO: GO:0003723; P:RNA binding; IEA.
 DR InterPro: IPR001363; Fetuin.
 DR PROSITE: PS01254; FETUIN_1; PARTIAL.
 DR PROSITE: PS01255; FETUIN_2; PARTIAL.
 KW RNA-binding.
 KW NON_TER 13 13
 SQ SEQUENCE 13 AA; 1370 MW; C683612A61757DC2 CRC64;

Query Match 35.3%; Score 18; DB 13; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYX 5
 |||
 Db 8 GYX 10

RESULT 6
 Q9TR07 PRELIMINARY; PRT; 14 AA.
 ID Q9TR07;
 AC Q9TR07;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Calcyclin-associated protein peptide L-8, CAP-50=ANNEXIN
 DE (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP MEDLINE=92317074; PubMed=1618851;
 RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
 RA Kobayashi R., Hidaka H.,
 RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
 fibroblast 3T3 cells."
 RL J. Biol. Chem. 267:13498-13504(1992).
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 14 AA; 1446 MW; C8322EB96DD9C6C6 CRC64;

Query Match 35.3%; Score 18; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred.No. 1.6e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFG 3
 DB 1 GFG 3

RESULT 7
 Q852V1 PRELIMINARY; PRT; 14 AA.
 ID Q852V1;
 AC Q852V1;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 OS Hydroxymethyltransferase-like protein (Fragment).
 CS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoidae; Andropogoneae; Zea.
 OC NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. C123;
 RA Ching A.S., Caldwell K.S., Jung M., Dolan M., Smith O.S., Tingey S.,
 RA Morgante M., Rafalski J.A.,
 RT "SNP frequency, haplotype structure and linkage disequilibrium in
 elite maize inbred lines."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DDJ databases.
 DR EMBL; AF498513; AAM1693.1;
 DR GO; GO:0008168; F: methyltransferase activity; IEA.
 DR GO; GO:0016740; F: transferase activity; IEA.
 KW Transferase; Methyltransferase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 14 AA; 1676 MW; 4741A2BD79E8E8P17 CRC64;

Query Match 35.3%; Score 18; DB 10; Length 14;
 Best Local Similarity 33.3%; Pred.No. 1.6e+04;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 GFGYKSKF 9
 DB 4 GFTLBSMKY 12

RESULT 8
 Q86922 PRELIMINARY; PRT; 14 AA.
 ID Q86922;
 AC Q86922;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE IE18 (Fragment).
 GN IE.
 OS Human cytomegalovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Cytomegalovirus.

OX NCBI_TaxID=10359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95264483; PubMed=7745737;
 RA Kerry J.A., Sehgal A., Barlow S.W., Cavanaugh V.J., Fish K.,
 RA Nelson J.A., Stenberg R.M.,
 RT "Isolation and characterization of a low-abundance splice variant from
 the human cytomegalovirus major immediate-early gene region."
 RL J. Virol. 69:3868-3872(1995).
 DR EMBL; S78373; AAB34284.1;
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 14 AA; 1585 MW; 4A8320F23D94DEC3 CRC64;

Query Match 35.3%; Score 18; DB 12; Length 14;
 Best Local Similarity 100.0%; Pred.No. 1.6e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFG 3
 DB 9 GFG 11

RESULT 9
 Q85718 PRELIMINARY; PRT; 14 AA.
 ID Q85718;
 AC Q85718;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Reovirus serotype 1 S2 (Fragment).
 OS Reovirus (type 1 / strain lang).
 OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
 OC NCBI_TaxID=10884;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83017877; PubMed=7123853;
 RA Galliard R.K., Li J.K., Keene J.D., Joklik W.K.,
 RT "The sequences at the termini of four genes of the three reovirus
 serotypes."
 RL Virology 121:320-326(1982).
 DR EMBL; J02303; AAA47241.1;
 DR InterPro; IPR04317; Sigma_1_2.
 DR Pfam; PF03084; Sigma_1_2; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 14 AA; 1516 MW; 52F79D201BF900C7 CRC64;

Query Match 35.3%; Score 18; DB 12; Length 14;
 Best Local Similarity 100.0%; Pred.No. 1.6e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFG 3
 DB 12 GFG 14

RESULT 10
 P70007 PRELIMINARY; PRT; 14 AA.
 ID P70007;
 AC P70007;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Histone H4-1 (Fragment).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85160855; PubMed=4039007;
 RA Gargiulo G., Razvi F., Ruberti I., Mohr I., Morcel A.,
 RT "Chromatin-specific hypersensitive sites are assembled on a Xenopus

RT histone gene injected into Xenopus oocytes."
 RL J. Mol. Biol. 181:335-349 (1985).
 DR EMBL; M23777; AAA49757.1; -
 DR PIR; I51432; I51432.
 FT NON TER
 SQ SEQUENCE 14 AA; 1524 MW; 65A76B0A927B34B4 CRC64;

Query Match
 Best Local Similarity 35.3%; Score 18; DB 13; Length 14;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3
 DB 11 GFG 13

RESULT 11

Q8CG13 PRELIMINARY; PRT; 9 AA.

AC Q8CG13;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-UN-2003 (TREMBLrel. 24, Last annotation update)
 DE Glutamate receptor ionotropic N-methyl D-aspartate-like 1A
 DE (Fragment).
 GN GRIN1A.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J;
 RA Wyder K.S., Mohan Raj B.K., Sciorra L.J., Roginski R.S.;

RT "The mouse orthologue of the human ionotropic glutamate receptor-like
 gene (GRIN1A) maps to mouse chromosome 9."
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF462417; AA015648.1; -

DR EMBL; AF462416; AA015648.1; JOINED.

DR MGD; MGI:107282; Grin1a.

DR GO; GO:0004872; F:receptor activity; IEA.

KW Receptor.

FT NON TER 1

FT NON TER 9

SQ SEQUENCE 9 AA; 1091 MW; 6A91233EB059C3B CRC64;

Query Match
 Best Local Similarity 33.3%; Score 17; DB 11; Length 9;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSKF 9
 DB 1 NEKF 4

RESULT 12

Q9X533 PRELIMINARY; PRT; 10 AA.

AC Q9X533;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Periplasmic mercuric ion binding protein (Fragment).

GN MERP.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;
 RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=203A;
 RX MEDLINE=97208220; PubMed=9055422;
 RA Liebert C.A., Wireman J., Smith T., Summers A.O.;

RT "Phylogeny of mercury resistance (mer) operons of gram-negative
 bacteria isolated from the fecal flora of primates."
 RL Appl. Environ. Microbiol. 63:1066-1076 (1997).
 RN (2)

RP SEQUENCE FROM N.A.

RC STRAIN=209A;

RX MEDLINE=98027386; PubMed=9361435;

RA Wireman J., Liebert C.A., Smith T., Summers A.O.;

RT "Association of mercury resistance with antibiotic resistance in the
 gram-negative fecal bacteria of primates."
 RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
 RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN=209A;

RX MEDLINE=20568355; PubMed=1116334;

RA Liebert C.A., Watson A.L., Summers A.O.;

RT "The quality of merC, a module of the mer mosaic."
 RL J. Mol. Evol. 51:607-622 (2000).
 DR EMBL; AF120964; AAD23783.1; -

FT NON TER 1

SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match
 Best Local Similarity 33.3%; Score 17; DB 2; Length 10;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYNS 7
 DB 3 GYNS 7

RESULT 13

Q9X534 PRELIMINARY; PRT; 10 AA.

AC Q9X534;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE Periplasmic mercuric ion binding protein (Fragment).

GN MERP.

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83655;
 RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=742H;

RX MEDLINE=98027386; PubMed=9361435;

RA Wireman J., Liebert C.A., Smith T., Summers A.O.;

RT "Association of mercury resistance with antibiotic resistance in the
 gram-negative fecal bacteria of primates."
 RL Appl. Environ. Microbiol. 63:4494-4503 (1997).
 RN (3)

RP SEQUENCE FROM N.A.

RC STRAIN=742H;

RX MEDLINE=20568355; PubMed=1116334;

RA Liebert C.A., Watson A.L., Summers A.O.;

RT "The quality of merC, a module of the mer mosaic."
 RL J. Mol. Evol. 51:607-622 (2000).
 DR EMBL; AF120965; AAD23785.1; -

FT NON TER 1

SQ SEQUENCE 10 AA; 1093 MW; 3F526335A5A77B58 CRC64;

Query Match
 Best Local Similarity 33.3%; Score 17; DB 2; Length 10;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYKNS 7
||:|
DB 3 GYSS 7

RESULT 14

Q8HUB4 PRELIMINARY; PRT; 10 AA.

AC Q8HUB4; 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Anomobryum julaceum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Bryales; Bryaceae; Anomobryum.
OX NCBI_TaxID=67232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AJ607;
RA Pedersen N., Cox C., Hedenas L.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF546765; AAN62980.1; -.
DR GO:GO:0009507; Chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
FT 10 10
SQ SEQUENCE 10 AA; 1326 MW; 6314C32409C321B4 CRC64;

Query Match 33.3%; Score 17; DB 8; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 KNSKF 9
||:|
DB 2 KTKF 6

RESULT 15

Q47059 PRELIMINARY; PRT; 11 AA.

AC Q47059; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Acetyl ornithine decarboxylase (Fragment).
GN ARG1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83064529; PubMed=6292860;
RA Chavliar D., Piette J., Glansdorff N.;
RT "IS3 can function as a mobile promoter in E. coli.";
RL Nucleic Acids Res. 10:5335-5948 (1982).
DR EMBL; J01589; AAA23485.1; -.
DR PIR; I41138; I41138.11
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1181 MW; 93F0429162C05721 CRC64;

Query Match 33.3%; Score 17; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
||:|
DB 8 GFGY 11

RESULT 16

Q9NL65 PRELIMINARY; PRT; 11 AA.

AC Q9NL65; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE ASABF-delta (Fragment).
GN ASABF-DELTA.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RA Kato Y.;
RT "Ascaris suum asabf-delta gene, exon 2.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB029815; EAA89496.1; -.
FT NON_TER 1 1
FT 11 11
SQ SEQUENCE 11 AA; 1187 MW; 8BADDDCD1EAB5861 CRC64;

Query Match 33.3%; Score 17; DB 5; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
||:|
DB 3 GFGY 6

RESULT 17

Q94IR5 PRELIMINARY; PRT; 11 AA.

AC Q94IR5; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Nonspecific lipid transfer protein (Fragment).
OS Pinus radiata (Monterey pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3347;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRUTP9-1158055;
RA Jones D.F.;
RT "Genetic mapping of the lipid transfer protein gene family in Pinus radiata and Pinus taeda.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029028; AAK40266.1; -.
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1361 MW; 471B518D473AE727 CRC64;

Query Match 33.3%; Score 17; DB 10; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSKF 9
||:|
DB 8 NSOF 11

RESULT 18

Q9TTE3 PRELIMINARY; PRT; 12 AA.

AC Q9TTE3; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Glutathione peroxidase 5 (Fragment).
 GN GPX5.
 OS Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99449360; PubMed=10521050;
 RA Berant G.R., Marklund S., Hu Z.L., Rothchild M.F.,
 RT "Rapid communication: mapping of the glutathione-peroxidase-5 (GPX5)
 RT gene to pig chromosome 7.";
 RL J. Anim. Sci. 77:2855-2856(1999).
 DR EMBL; AF124818; AAF22118.1; -.
 DR GO; GO:0004601; F:peroxidase activity; IEA.
 KW Peroxidase.
 FT NON TER 1 1
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1307 MW; D4E39E8F50B451B6 CRC64;

 QY 1 GGGYKNS 7
 Db 2 GFVQTNS 8

 RESULT 19
 O8HU93 PRELIMINARY; PRT; 12 AA.
 AC O8HU93;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN Pili6.
 OS Bryum donianum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Bryopsida; Bryidae; Bryales; Bryaceae; Bryum.
 OX NCBI_TaxID=66993;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BD528;
 RA Pedersen N., Cox C., Hedenas L.,
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF546786; AAN63001.1; -.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON TER 1 1
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1539 MW; 5F27C314C32409C3 CRC64;

 QY 5 KNSKF 9
 Db 2 KRTKF 6

 RESULT 20
 O47601 PRELIMINARY; PRT; 13 AA.
 AC O47601;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE C (Fragment).
 GN C.

OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91139577; PubMed=1995588;
 RA Tao T., Bourne J.C., Blumenhal R.M.,
 RT "A family of regulatory genes associated with type II restriction-
 RT modification systems.";
 RL J. Bacteriol. 173:1367-1375(1991).
 DR EMBL; M63620; AAA24557.1; -.
 FT NON TER 1 1
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1485 MW; DABCB136F902866 CRC64;

 QY 3 GYNSX 8
 Db 7 GLKNEQ 12

 RESULT 21
 P82808 PRELIMINARY; PRT; 13 AA.
 ID P82808;
 AC P82808;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Glucosamine-6-phosphate-6-phosphate aminotransferase [isomerizing]
 DE (EC 2.6.1.16) (Hexosephosphate aminotransferase (D-fructose-6-
 DE phosphate aminotransferase) (GPA) (Fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=20358980; PubMed=10898949;
 RA Huynh O.K., Guive E.A., Dian T.;
 RT "Purification and characterization of glutamine:fructose 6-phosphate
 RT aminotransferase from rat liver.";
 RL Arch. Biochem. Biophys. 379:307-313 (2000).
 CC -1- FUNCTION: CONTROLS THE FLUX OF GLUCOSE INTO THE HEXOSAMINE
 CC PATHWAY. MOST LIKELY INVOLVED IN REGULATING THE AVAILABILITY OF
 CC PRECURSORS FOR N- AND O-LINKED GLYCOSYLATION OF PROTEINS.
 CC -1- CATALYTIC ACTIVITY: L-GLUTAMINE + D-FRUCTOSE 6-PHOSPHATE =
 CC L-GLUTAMATE + D-GLUCOSAMINE 6-PHOSPHATE.
 CC -1- ENZYME REGULATION: INHIBITED BY 4',4'-DITHIOPYRIDINE.
 CC -1- PATHWAY: FIRST AND RATE-LIMITING ENZYME OF THE HEXOSAMINE
 CC BIOSYNTHETIC PATHWAY.
 CC -1- SUBUNIT: HOMOTETRAMER (POTENTIAL).
 CC -1- MISCELLANEOUS: ITS OPTIMUM PH IS 7.5.
 CC -1- SIMILARITY: STRONG, TO OTHER GPA.
 CC -1- SIMILARITY: THE GATASE DOMAIN BELONGS TO TYPE-2 GLUTAMINE
 CC AMIDOTRANSFERASES.
 DR GO; GO:0004360; F:glutamine-fructose-6-phosphate transaminase. . .; IEA.
 DR GO; GO:0016740; F:glutaminase activity; IEA.
 DR GO; GO:0006541; P:glutamine metabolism; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR InterPro; IPR000583; GATase 2.
 DR PROSITE; PS00443; GATASE TYPE_II; 1.
 KW Transferase; Aminotransferase; Glutamine amidotransferase.
 FT INIT MET 0 0
 FT ACT SITE 1 1
 FT DOMAIN 1 1
 FT NON TER 13 13
 SQ SEQUENCE 13 AA; 1553 MW; 0944F6BB32DB473B CRC64;

Query Match 33.3%; Score 17; DB 11; Length 13;
Best Local Similarity 60.0%; Pred. No. 2.3e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGYN 6
DB 4 FAYLN 8

RESULT 22

07X4C1 PRELIMINARY; PRT; 8 AA.
AC 07X4C1;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Ribosomal protein S19 (Fragment).
GN RPS19.
OS Potato witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phytoplasma.
OX NCBI_TaxID=37701;
RN SEQUENCE FROM N.A.
RP STRAIN=PMB;
RA Lee I.-M., Martini M., Marcone C., Zhu S.;
RT "Classification of phytoplasma strains in the elm yellows group (16SIV) and proposition of 'Candidatus Phytoplasma umii' for the RT phytoplasma associated with elm yellows and 'Candidatus Phytoplasma chrysanthemi' for the phytoplasma associated with cherry lethal yellowing in China."
RL Submitted (DEC-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY197682; AAP42406.1; -.
KW Ribosomal protein.
FT NON_TER
SQ SEQUENCE 8 AA; 945 MW; 783326D443333AA8 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 KNSK 8
DB 4 KNOX 7

RESULT 23

09BYF9 PRELIMINARY; PRT; 9 AA.
AC 09BYF9;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 24, Last annotation update)
DE Cytochrome c19 (Fragment).
GN K19.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A.
RP MEDLINE=21539745; PubMed=11682035;
RA Kagaya M., Kaneko S., Ono H., Inamura K., Kobayashi K.;
RT "Cloning and characterization of the 5'-flanking region of human cytochrome c19 gene in human cholangiocarcinoma cell line."
RL J. Hepatol. 35:504-511 (2001).
DR EMBL: AB045973; BAB40770.1; -.
DR GO: GO:0005882; C:intermediate filament; IEA.
KW Keratin.
FT NON_TER
SQ SEQUENCE 9 AA; 1122 MW; 9E9FC41B45BA5A1 CRC64;

Query Match 31.4%; Score 16; DB 4; Length 9;

Best Local Similarity 33.3%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGYN 7
DB 4 YSYROS 9

RESULT 24

054217 PRELIMINARY; PRT; 10 AA.
AC 054217;
DT 01-JUN-1998 (TRENBLrel. 06, Created)
DT 01-JUN-1998 (TRENBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Transposase (Fragment).
GN TNP1.
OS Staphylococcus epidermidis.
OG Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN SEQUENCE FROM N.A.
RP STRAIN=BN 280;
RX MEDLINE=98394975; PubMed=9726851;
RA Heidrich C., Pag U., Josten M., Metzger J., Jack R.W., Bierbaum G., Jung G., Sahl H.G.;
RT "Isolation, characterization and sequence of the novel lantibiotic RT epididym 280 and its biosynthetic gene cluster."
RL Appl. Environ. Microbiol. 64:3140-3146 (1998).
DR EMBL: Y14023; CAA74345.1; -.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
KW Plasmid.
FT NON_TER
SQ SEQUENCE 10 AA; 1453 MW; 05A0EFD32B4409DB CRC64;

Query Match 31.4%; Score 16; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYN 5
DB 4 FRYK 7

RESULT 25

086580 PRELIMINARY; PRT; 10 AA.
AC 086580;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Large protein (Fragment).
GN Simian parainfluenza virus 5.
OS Viruses; ssRNA negative-strand viruses; Mononegavirales; Paramyxoviridae; Paramyxovirinae; Rubulavirinae.
OX NCBI_TaxID=11207;
RN SEQUENCE FROM N.A.
RP MEDLINE=93224905; PubMed=8385701;
RA Higuchi Y., Miyahara Y., Kawano M., Tsurudome K., Matsumura H., Kuesgawa S., Komada H., Nishio M., Ito Y.;
RT "Sequence analysis of the large (L) protein of simian virus 5."
RL J. Gen. Virol. 74:789-789 (1993).
DR EMBL: S57860; AAB26118.1; -.
FT NON_TER
SQ SEQUENCE 10 AA; 1144 MW; 0C25A0D9C86776D4 CRC64;

Query Match 31.4%; Score 16; DB 12; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.7e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 6

Db 6 GFCN 9

RESULT 26

Q9UR95 PRELIMINARY; PRT; 11 AA.

AC Q9UR95;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Heat shock protein 60 homolog (Fragment).
OS Pichia angusta (Yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Pichia.
OX NCBI_TaxID=4905;
RN [1]
RP SEQUENCE.
RX MEDLINE=93223840; PubMed=8096822;
RA Everts W.E., Hulse B., Tilotenko V.I., Kunau W.H., Hartl F.U.,
RT "Affinity purification of molecular chaperones of the yeast Hansenula
polymorpha using immobilized denatured alcohol oxidase."
RL FEMS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C372B CRC64;

Query Match 31.4%; Score 16; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YNSKF 9
2 HKELKP 7

RESULT 27

Q89616 PRELIMINARY; PRT; 11 AA.

AC Q89616;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Avian infectious bronchitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11120;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87111468; PubMed=3027249;
RA Boursnell M.E., Brown T.D.K., Foulds I.J., Green P.F., Tomley F.M.,
RT "Completion of the sequence of the genome of the coronavirus avian
infectious bronchitis virus."
RL J. Gen. Virol. 68:57-77(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88130171; PubMed=2829522;
RA Boursnell M.E., Brown T.D., Foulds I.J., Green P.F., Tomley F.M.,
RT "The complete nucleotide sequence of avian infectious bronchitis
virus: analysis of the polymerase-coding region."
RL Adv. Exp. Med. Biol. 218:15-29(1987).
DR EMBL; M27471; AAA4622.1; -.
DR EMBL; M27471; AAA4622.1; -.
KW Hypothetical protein.

QY SEQUENCE 11 AA; 1182 MW; 251E3F165B721B CRC64;

Query Match 31.4%; Score 16; DB 12; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4

Db 8 GFCY 11

RESULT 28

Q9S8F0 PRELIMINARY; PRT; 12 AA.

AC Q9S8F0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Glutathione S-transferase isoform II (EC 2.5.1.18) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RX MEDLINE=95322859; PubMed=7599527;
RA Holt D.C., Lay V.J., Clarke E.D., Dinsmore A., Jepson I., Bright S.W.,
RT "Characterization of the safener-induced glutathione S-transferase
isoform II from maize."
RL Planta 196:295-302(1995).
DR GO; GO:0004364; F:Glutathione transferase activity; IBA.
SQ SEQUENCE 12 AA; 1382 MW; C28977F65975B05D CRC64;

Query Match 31.4%; Score 16; DB 10; Length 12;
Best Local Similarity 37.5%; Pred. No. 3.2e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 FGYSKF 9
2 YGWAISPF 9

RESULT 29

Q9U5J3 PRELIMINARY; PRT; 13 AA.

AC Q9U5J3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Heat shock protein 100 (Fragment).
GN HSP100.
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ILTARI;
RA Webb H.D., Gaud A.F., Carrington M.,
RT "The trypanosoma brucei GPI-PLC gene is not linked to functionally
related genes or to genes showing the same developmentally regulated
RT expression."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; A0250727; CAB60092.1; -.
FT NON_TER

QY SEQUENCE 13 AA; 1524 MW; 37C19EC3787FA728 CRC64;

Query Match 31.4%; Score 16; DB 5; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 FGYSK 5
1 FGVS 4

RESULT 30

Q9NC73 PRELIMINARY; PRT; 13 AA.

AC Q9NC73.
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Putative ABC transporter (Fragment).
 OS Oxytricha trifallax (Stekkiella histriomuscorum).
 CC Eukaryota; Alveolata; Ciliophora; Spirotrichea; Stichotrichia;
 CC Stichotrichida; Oxytrichidae; Stekiella.
 NCBI_TaxID=94289;
 OX NCBI [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BA;
 RC Villalobo E., Moch C., Perasso R., Baroin-Tourancheau A.;
 RA "differential display analysis of gene expression in Stekiella
 RT histriomuscorum (Ciliophora, Oxytrichidae). Characterization of an
 RT excystment-associated up-regulated ABC transporter encoding-gene."
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF231990; AAF87978.1; -
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1387 MW; 3EBB181F6153D698 CRC64;

Query Match 31.4%; Score 16; DB 5; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3.4e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 GYKNSK 8
 DB 6 GYKNSK 11

RESULT 31
 Q29823 PRELIMINARY; PRT; 13 AA.
 AC Q29823;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE ORF 1 protein.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_TaxID=9606;
 OX NCBI [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=96144827; PubMed=856858;
 RA Beck S., Abdulla S., Alderton R.P., Glynn R.J., Gut I.G.,
 RA Hosking L.K., Jackson A., Kelly A., Newell W.R., Sansau P.,
 RA Radley E., Thorpe K.L., Trowsdale J.;
 RT "evolutionary dynamics of non-coding sequences within the class II
 RT region of the human MHC."
 RL J. Mol. Biol. 255:1-13(1996).
 DR EMBL; X87344; CAA60783.1; -
 SQ SEQUENCE 13 AA; 1512 MW; 1F89485D7E9CA5B4 CRC64;

Query Match 31.4%; Score 16; DB 7; Length 13;
 Best Local Similarity 75.0%; Pred. No. 3.4e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 NSKF 9
 DB 8 SSKF 11

RESULT 32
 Q7X9Y2 PRELIMINARY; PRT; 13 AA.
 ID Q7X9Y2;
 AC Q7X9Y2;
 DT 01-OCT-2003 (TRENBLrel. 25, Created)
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE TAG1 (Fragment).
 GN Lycopodium esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 NCBI_TaxID=4081;
 OX NCBI [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=cv. Micro-Tomato;
 RC MEDLINE=22667639; PubMed=12782724;
 RA Hong R.L., Haseguchi U., Busch M.A., Weigel D.;
 RT "Regulatory Elements of the Floral Homeotic Gene AGAMOUS Identified by
 RT Phylogenetic Footprinting and Shadowing."
 RL Plant Cell 15:1296-1309(2003).
 DR EMBL; AY254705; AAB5239.1; -
 FT NON TER 1
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1598 MW; CA858C01E9E44D CRC64;

Query Match 31.4%; Score 16; DB 10; Length 13;
 Best Local Similarity 28.6%; Pred. No. 3.4e+04;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 FGKNSK 8
 DB 3 YEVANNR 9

RESULT 33
 Q8KSE3 PRELIMINARY; PRT; 14 AA.
 ID Q8KSE3;
 AC Q8KSE3;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE Truncated protein kinase.
 GN VANS.
 OS Enterococcus faecium (Streptococcus faecium).
 CC Plasmid pUW786.
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 NCBI_TaxID=1352;
 OX NCBI [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=UW786;
 RC Werner G., Klare I., Witte W.;
 RT "Multi-resistance gene cluster on a plasmid in a clinical isolate of
 RT Enterococcus faecium."
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516315; AAM77883.1; -
 DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0016301; F:kinase activity; IEA.
 KW Kinase; Plasmid.
 SQ SEQUENCE 14 AA; 1628 MW; 0AAE44BCDE720A34 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3.7e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 KNSK 8
 DB 6 KNSK 9

RESULT 34
 Q94IT6 PRELIMINARY; PRT; 14 AA.
 ID Q94IT6;
 AC Q94IT6;
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Regulator of anthocyanin biosynthesis pathway (Fragment).
 OS Fragaria nubicola.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.

OX NCBI_TaxID=60188;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. FRA520;
 RA Deng C., Davis T.;
 RT "Molecular identification of the yellow fruit color (c) locus in
 RL diploid strawberry: a candidate gene approach."
 DR EMBL; AY017488; AAK3145.1; --
 FT NON_TER
 SQ SEQUENCE 14 AA; 153 MW; C2862BA5812DC832 CRC64;

Query Match
 Best Local Similarity 31.4%; Score 16; DB 10; Length 14;
 Pred. No. 3.7e+04;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
 DB 11 GDGY 14

RESULT 35
 O945F2 PRELIMINARY; PRT; 14 AA.
 AC O945F2;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 OS Aldolase (Fragment).
 OC Cicer arerium (Chickpea) (Garbanzo).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids 1; Fabales; Fabaceae; Papilionoideae; Ciceraceae; Cicer.
 OX NCBI_TaxID=3827;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rajesh P.N., Gupta V.S., Ranjekar P.K., Muehlbauer F.J.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF416480; AAL08017.1; --
 FT NON_TER
 SQ SEQUENCE 14 AA; 1785 MW; 421376873P9353C7 CRC64;

Query Match
 Best Local Similarity 31.4%; Score 16; DB 10; Length 14;
 Pred. No. 3.7e+04;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
 DB 11 GYSY 14

RESULT 36
 O9UJ50 PRELIMINARY; PRT; 8 AA.
 AC O9UJ50;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99153747; PubMed=10030676;
 RA White G.R.M., Varley J.M., Heigway J.;
 RT "Isolation and characterization of a human homologue of the
 RT latrophilin gene from a region of 1p31.1 implicated in breast
 RT cancer."
 RL Oncogene 17:3513-3519(1998).

RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20225451; PubMed=10760572;
 RA White G.R.M., Varley J.M., Heigway J.;
 RT "Genomic structure and expression profile of lPHN1, a 7TM gene
 RT variably expressed in breast cancer cell lines."
 RL Biochim. Biophys. Acta 1491:75-92(2000).
 DR EMBL; AJ244509; CAB60204.1; --
 FT NON_TER
 SQ SEQUENCE 8 AA; 1025 MW; 4D59D763344AAB0B CRC64;

Query Match
 Best Local Similarity 29.4%; Score 15; DB 4; Length 8;
 Pred. No. 1e+06;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 YKNSK 8
 DB 1 YEDNK 5

RESULT 37
 O8GDC0 PRELIMINARY; PRT; 10 AA.
 AC O8GDC0;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 OS Sulfolobus solfataricus (Fragment).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Neomarkis I.K., Scoulis E.V., Tselentis Y.J.;
 RT "First detection of Diarrhoea in an Escherichia coli clinical
 RT isolate."
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY152821; AAN77716.1; --
 FT NON_TER
 SQ SEQUENCE 10 AA; 1106 MW; 91F57E205879D2D1 CRC64;

Query Match
 Best Local Similarity 29.4%; Score 15; DB 2; Length 10;
 Pred. No. 4e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 FGYN 6
 DB 5 FGLN 9

RESULT 38
 O9UN90 PRELIMINARY; PRT; 10 AA.
 AC O9UN90;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tanaka T., Uchiyama T., Hinoshita E., Inokuchi A., Toh S., Wada M.,
 RA Nomoto M., Kohno K., Kuwano M.;
 RT "Sequence analysis and functional characterization of the 5'-flanking
 RT region of the human canalicular multispecific organic anion
 RT transporter/multidrug resistance protein 2 (cMOAT/MRP2) gene."

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL, AF144630; AAD47599.1; -.

FT NON TER 10 10

SQ SEQUENCE 10 AA; 1219 MW; 76F28CB44EB9C3B CRC64;

Query Match 29.4%; Score 15; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 4e+04;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSKF 9

Db 7 NSTF 10

RESULT 39

Q26093 PRELIMINARY; PRT; 10 AA.

AC Q26093; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

H2B (10 AA) (Fragment).

Pisaster ochraceus (Sea star).

OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Asterozoa;

OC Ascoridida; Forcipulatacea; Forcipulata; Asteriidae; Pisaster.

NCBI_TaxID=7612;

SEQUENCE FROM N.A.

RC Tissue-Sperm; Cool D., Hewitt J., Ydenberg B., Smith M.J., Honda B.M.;

RA Howell A.M., "Organization and Unusual Expression of Histone Genes in the Sea Star

RT Pisaster ochraceus";

RL J. Mol. Evol. 25:29-36(1987).

DR EMBL; X05620; CAA29107.1; -.

FT NON TER 1 1

SQ SEQUENCE 10 AA; 1126 MW; DD7806B1BB5321B2 CRC64;

Query Match 29.4%; Score 15; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 4e+04;

Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YKNSK 8

Db 6 YTTSK 10

RESULT 40

Q25916 PRELIMINARY; PRT; 11 AA.

AC Q25916; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

Malaria antigen (7H8/2) (Fragment).

OC Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=5833;

SEQUENCE FROM N.A.

Db 8 YKNSK 10

RESULT 41

Q9GH12 PRELIMINARY; PRT; 11 AA.

AC Q9GH12; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

Photosystem II CP43 apoprotein (Fragment).

PSBC.

OC Pandorina morum.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;

OC Volvocaceae; Pandorina.

NCBI_TaxID=33099;

SEQUENCE FROM N.A.

RC STRAIN=DTEX 2326;

RA MEDLINE=20538271; PubMed=11083939;

RA Nozaki H., Misawa K., Kajita T., Kato M., Nohara S., Matanabe M.M.;

RT "Origin and Evolution of the Colonial Volvocales (Chlorophyceae) as

RT Inferred from Multiple Chloroplast Gene Sequences.";

RL Mol. Phylogenet. Evol. 17:256-268(2000).

DR EMBL; AB044506; BAB18432.1; -.

GO; GO:0009507; C:Chloroplast; IEA.

FT NON TER 1 1

SQ SEQUENCE 11 AA; 1140 MW; 04E525247731ADD0 CRC64;

Query Match 29.4%; Score 15; DB 8; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.4e+04;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3

Db 8 GYG 10

RESULT 42

Q32704 PRELIMINARY; PRT; 11 AA.

AC Q32704; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

NdhB protein (Fragment).

OC Nicotiana tabacum (Common tobacco).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Solanales; Solanaceae; Nicotiana.

NCBI_TaxID=4097;

SEQUENCE FROM N.A.

RC STRAIN=Brict yellow 4; TISSUE=leaf;

RA MEDLINE=86210537; PubMed=3329576;

RA Hayashida N., Matsubayashi T., Shinzaki K., Sugitara M., Inoue K.,

RA "The gene for the 9kd polypeptide, a possible apoprotein for the iron-

RT sulfur centers A and B of the photosystem I complex in tobacco

RT chloroplast DNA.";

RL Curr. Genet. 12:247-250(1987).

DR EMBL; X05881; CAA29303.1; -.

GO; GO:0009507; C:chloroplast; IEA.

FT NON TER 1 1

SQ SEQUENCE 11 AA; 1338 MW; 008165EE304776CB CRC64;

Query Match 29.4%; Score 15; DB 8; Length 11;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3

Db 8 GYG 10

RESULT 42

Q32704 PRELIMINARY; PRT; 11 AA.

AC Q32704; 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

NdhB protein (Fragment).

OC Nicotiana tabacum (Common tobacco).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;

OC Lamiales; Solanales; Solanaceae; Nicotiana.

NCBI_TaxID=4097;

SEQUENCE FROM N.A.

RC STRAIN=Brict yellow 4; TISSUE=leaf;

RA MEDLINE=86210537; PubMed=3329576;

RA Hayashida N., Matsubayashi T., Shinzaki K., Sugitara M., Inoue K.,

RA "The gene for the 9kd polypeptide, a possible apoprotein for the iron-

RT sulfur centers A and B of the photosystem I complex in tobacco

RT chloroplast DNA.";

RL Curr. Genet. 12:247-250(1987).

DR EMBL; X05881; CAA29303.1; -.

GO; GO:0009507; C:chloroplast; IEA.

FT NON TER 1 1

SQ SEQUENCE 11 AA; 1338 MW; 008165EE304776CB CRC64;

Query Match 29.4%; Score 15; DB 8; Length 11;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFG 3

Db 8 GYG 10

Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YKNSKF 9
DB 4 YQPIKF 9

RESULT 43

O9QVH3 PRELIMINARY; PRT; 11 AA.

AC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chromogranin-B, CGB=GLUCAGONOMA peptide (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92063871; PubMed=1954695;
RA Nielsen E., Melinder B.S., Madson O.D.;
RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma
peptides through processing at mono-, di-, or tribasic residues.";
RL Endocrinology 129:3147-3156(1991).
DR InterPro; IPR001990; Granin.
DR Pfam; PF01271; Granin; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1342 MW; 6C82C3737452CAB CRC64;

Query Match 29.4%; Score 15; DB 11; Length 11;
Best Local Similarity 50.0%; Pred. No. 4.4e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 FGXX 5
DB 8 WGYE 11

RESULT 44

O8KH47 PRELIMINARY; PRT; 12 AA.

AC 08KH47;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Putative transposase (Fragment).
OS Enterococcus faecium (Streptococcus faecium).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TUH2-18, and TUH2-21;
RA Dahl K.H., Roekens T.P., Lundblad B.W., Midvedt T., Sundsfjord A.;
RT "Heterogeneity in horizontal transfer of vanB-type vancomycin-
resistance and molecular evidence for transposition of the vanB2-
containing transposon, Tn382, in clinical Enterococcus faecium
isolates.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289473; AAM92720.1; -
DR EMBL; AF289474; AAM92721.1; -
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1497 MW; F270AFB8017339C1 CRC64;

Query Match 29.4%; Score 15; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 4.7e+04;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 YKNSKF 9
DB 4 YQPIKF 9

DB 6 FRGKQF 11

RESULT 45

O53579 PRELIMINARY; PRT; 12 AA.

AC 053579;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Light-harvesting complex I alpha polypeptide (Fragment).
GN PUFA.
OS Rhodospirillum rubrum (Rhodospirillum rubrum capsulata).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Rhodospirillum.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92234963; PubMed=1569029;
RA Richter P., Brand M., Drews G.;
RT "Characterization of LHT- and LHT+ Rhodospirillum rubrum
mutants.";
RL U. Bacteriol. 174:3030-3041(1992).
DR EMBL; S97551; AAC60405.1; -
FT NON_TER 12
FT NON_TER 12
SQ SEQUENCE 12 AA; 1627 MW; 0F92FEA8A70532B CRC64;

Query Match 29.4%; Score 15; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 SKF 9
DB 2 SKF 4

Search completed: August 30, 2004, 10:55:16
Job time: 11.6655 secs

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OM protein - protein search, using sw model

Run on: August 30, 2004, 10:40:09 / Search time 1.55068 Seconds
(without alignments)
302.211 Million cell updates/sec

Title: US-09-720-469A-3
Perfect score: 51
Sequence: 1 GFGYKSKF 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 585

Minimum DB seq length: 8
Maximum DB seq length: 14

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	41.2	13	1 ORCK_ORCLI	P37086 orconectes
2	20	39.2	10	1 FAR7_MACRS	P83280 macrobrachi
3	20	39.2	10	1 HTP_TABAT	P14596 tabanus atr
4	20	39.2	13	1 LMA1_LOCM1	P34966 locustea mig
5	19	37.3	10	1 CU30_LOCM1	P11735 locustea mig
6	19	37.3	10	1 TXMB_RANCA	P22689 rana catesb
7	19	37.3	12	1 FAR7_PENMO	P83322 penaeus mon
8	18	35.3	11	1 CX14_CONNR	P58807 conus marino
9	18	35.3	13	1 CX14_CONNR	P58810 conus marino
10	17	33.3	9	1 FARP_CALSI	P36495 callinectes
11	17	33.3	11	1 NXSN_PSETE	P59072 pseudonaja
12	16	31.4	12	1 TA10_TREME	P01371 tremella me
13	16	31.4	14	1 RS19_CLOPB	O46228 clover prol
14	16	31.4	14	1 RS19_CLOPB	O46878 loofah wite
15	15	29.4	8	1 RS1_ERWCH	P37985 erwina chr
16	15	29.4	9	1 FAR9_ASCSU	P43172 ascaris suu
17	15	29.4	10	1 TKU2_UREUN	P40752 urechis uni
18	15	29.4	11	1 CA42_LITCI	P82092 litorea cit
19	15	29.4	11	1 TKC2_CALVO	P41518 calliphora
20	15	29.4	11	1 GRAR_RANRU	P40754 rana rugosa
21	15	29.4	12	1 NP1_LYNST	P80178 lymanaea sta
22	15	29.4	13	1 NP4_LYNST	P80181 lymanaea sta
23	15	29.4	13	1 TEM1_RANTE	P57104 rana tempor
24	15	29.4	13	1 MY14_EISFO	P46879 eisenia foe
25	15	29.4	14	1 RS19_PWBMP	O52993 pigeon pea
26	15	29.4	14	1 SMS1_MYOSC	P20750 myoxocephal
27	15	29.4	14	1 SMS1_MYOSC	P31885 alligator m
28	15	29.4	8	1 LCK5_LEUMA	P19887 leucophaea
29	14	27.5	9	1 STAP_XUSCA	P19095 mustelus ca
30	14	27.5	10	1 FAR2_PENMO	P83317 penaeus mon
31	14	27.5	10	1 RL16_ACHLA	P29221 acholeplaeam
32	14	27.5	11	1 EFG_CLOPA	P81550 clostridium
33	14	27.5	12	1 RS19_CLYEP	O46490 clover yell

34	14	27.5	12	1 RS19_TOBRP	O56251 tomato big
35	14	27.5	13	1 IDHC_PIG	P20304 sus scrofa
36	14	27.5	13	1 NEUT_CAVPO	P32860 cavia porce
37	14	27.5	14	1 UC18_MAIZE	P80624 zea mays (m
38	13.5	26.5	13	1 SA2B_ONCMY	P82238 oncornyrchu
39	13.5	26.5	13	1 SA2B_ONCMY	P82239 oncornyrchu
40	13	25.5	8	1 AL15_CYPDO	P82156 cydia pomon
41	13	25.5	9	1 NEF_FV1Z8	P12481 human immun
42	13	25.5	9	1 NEUT_CAVPO	P34866 cavia porce
43	13	25.5	9	1 NSK1_SARBU	P41492 sarcophaga
44	13	25.5	10	1 ESTA_SCHGA	P81012 schizaphis
45	13	25.5	10	1 HTP_HELIZE	P16353 heliothis z

ALIGNMENTS

RESULT 1
ORCK_ORCLI STANDARD; PRT; 13 AA.
ID ORCK_ORCLI
AC P37086;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Orckorlin.
OS Orconectes limosus (Spinycheek crayfish).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Astacoidae; Cambaridae; Orconectes.
OX NCBI_TaxID=28379;
RN [1]
RP SEQUENCE.
RC TISSUE=Abdominal nerve cord;
RX MEDLINE=3126144; Pubmed=1480511;
RA Stangier J., Hildrich C., Burdzik S., Keller R.;
RT "Orckorlin: a novel myotropic peptide from the nervous system of the
crayfish, Orconectes limosus.";
RL Peptides 13:859-864(1992).
CC -1- FUNCTION: Myotropic peptide; enhances both the frequency and
amplitude of spontaneous hindgut contractions.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Abdominal nerve cord and hindgut.
KW Neuropeptide.
SQ SEQUENCE 13 AA; 1518 MW; 8A31B7BA93A40A CRC64;
QY 1 GFGY 4
Db 9 GFGF 12
Query Match 41.2%; Score 21; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
RESULT 2
FAR7_MACRS STANDARD; PRT; 10 AA.
ID FAR7_MACRS
AC P83280;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Macrobrachium rosenbergii (Giant fresh water prawn).
OS Macrobrachium rosenbergii (Giant fresh water prawn).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC Palaemonoidea; Palaemonidae; Macrobrachium.
OX NCBI_TaxID=79674;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Esophageal;
RX MEDLINE=21107394; Pubmed=11179812;
RA Stihlgornul P., Sarathongkum W., Longyant S., Panchan N.,
Stihlgornul W., Peterson A.;

RT "Three more novel FMRFamide-like neuropeptide sequences from the
RT eyestalk of the giant freshwater prawn *Macrobrachium rosenbergii*."
RL Peptides 22:191-197(2001).
CC -1- MASS SPECTROMETRY: MW=1244.9; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
DR GO:0007218; P-neuropeptide signaling pathway; IDA.
KM Neuropeptide; Amidation.
FT MOD RES 10
SQ SEQUENCE 10 AA; 1244 MW; 3CFE9C29C4540A8 CRC64;
Query Match 39.2%; Score 20; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 GFGY 6
DB 1 GYGRN 6

RESULT 3
HTF_TABAT STANDARD; PRT; 10 AA.
ID HTF_TABAT
AC P14596;
DT 01-JAN-1990 (Rel. 13, Created)
DR 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypertrehalosemic factor (HOTH) (Dipteran corpora cardiaca factor II)
DS (DCC II).
OS Tabanus atratus (Horse fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Tabanomorpha; Tabanidae;
OC Tabanus.
OX NCBI_TaxID=7207;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA MEDLINE=90046758; PubMed=2813385;
RX Jaffe H., Raina A.K., Riley C.T., Fraser B.A., Nachman R.J.,
RA Vogel V.W., Zhang Y.-S., Hayes D.K.;
RT "Primary structure of two neuropeptide hormones with adipokinetic and
RT hypertrehalosemic activity isolated from the corpora cardiaca of horse
RT files (Diptera)."
RL Proc. Natl. Acad. Sci. U.S.A. 86:8161-8164(1989).
CC -1- FUNCTION: Hypertrehalosemic factors are neuropeptides that
CC elevate the level of trehalose in the hemolymph (trehalose is the
CC major carbohydrate in the hemolymph of insects).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC PIR, B33995; B33995.
DR InterPro; IPR002047; ANH.
DR PROSITE; PS00256; AKH; 1.
KM Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD RES 10
FT MOD RES 10
SQ SEQUENCE 10 AA; 1169 MW; 916036786771A9D1 CRC64;
Query Match 39.2%; Score 20; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 1 GFGY 4
DB 7 GMY 10

RESULT 4
LMAL_LOCM1 STANDARD; PRT; 13 AA.
ID LMAL_LOCM1
AC P38496;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Lom-Ag-myotropin I (accessory gland myotropin I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caellifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Male accessory gland;
RA MEDLINE=91271087; PubMed=2052501;
RX Paemen L., Tjies A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Lom-Ag-myotropin: a novel myotropic peptide from the male accessory
RT glands of *Locusta migratoria*."
RL Peptides 12:7-10(1991).
CC -1- FUNCTION: The exact physiological function is still unknown. This
CC myotropic peptide is active on the oviduct and, to a lesser
CC extent, on the hindgut. Transferred from the male to the female
CC during copulation.
CC -1- TISSUE SPECIFICITY: Male accessory glands.
KM Neuropeptide; Amidation.
FT MOD RES 13
FT MOD RES 13
SQ SEQUENCE 13 AA; 1368 MW; DE1ACAFCA82B72D CRC64;
Query Match 39.2%; Score 20; DB 1; Length 13;
Best Local Similarity 75.0%; Pred. No. 6.8e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 GYRN 6
DB 1 GYGRN 4

RESULT 5
CU30_LOCM1 STANDARD; PRT; 10 AA.
ID CU30_LOCM1
AC P11735;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cuticle protein 30 (LM-30) (LM-ACP 30) (Fragment).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caellifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=86109304; PubMed=3943519;
RA Hoelrup P., Andersen S.O., Roepstorff P.;
RT "Isolation, characterization, and N-terminal sequence studies of
RT cuticular proteins from the migratory locust, *Locusta migratoria*."
RL Eur. J. Biochem. 154:153-159(1986).
CC -1- FUNCTION: Component of the cuticle of migratory locust which
CC contains more than 100 different structural proteins.
KM PIR; H24802; H24802.
DR Structural protein; Cuticle.
FT NON TER 10
FT NON TER 10
SQ SEQUENCE 10 AA; 969 MW; 4973E36B58772877 CRC64;
Query Match 37.3%; Score 19; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.1e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 GFGY 4
DB 4 GYGRN 7

RESULT 6
TKXB_RANCA STANDARD; PRT; 10 AA.
ID TKXB_RANCA
AC P22689;
DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ranachykinin B (RTK B).
 OS Rana catesbeiana (Bull Frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_Taxid=8400;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain; PubMed=2043143;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana)
 brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-595(1991).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Intestine; PubMed=8210506;
 RX MEDLINE=94023216; PubMed=8210506;
 RA Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and
 intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC -1- FUNCTION: Tachykinins are active peptides which excite neurons,
 evoke behavioral responses, are potent vasodilators and
 secretagogues, and contract (directly or indirectly) many smooth
 muscles.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the tachykinin family.
 DR PIR, B61033; B61033. Tachy. Neurokinin.
 DR InterPro; IPR002040; Tachy. Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1210 MW; 917E55B5859D5B45 CRC64;

Query Match 37.3%; Score 19; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 8.1e+02;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YKNSKF 9
 ||:
 1 YKDSDF 6

RESULT 7
 FAR7 PENMO STANDARD; PRT; 12 AA.
 ID FAR7 PENMO
 AC P83322;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE FMRFamide-like neuropeptide Flp7 (GYRPPNNSIF-amide).
 OS Penaeus monodon (Penaeid shrimp).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 CC Penaeidae; Penaeus.
 OX NCBI_Taxid=6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk; PubMed=11959015;
 RX MEDLINE=21956277; PubMed=11959015;
 RA Sithigorngul P., Pupum J., Krungkarn C., Longyant S.,
 RA Chaisrihangkura P., Sithigorngul W., Petson A.;
 RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn Penaeus monodon.";
 RL Comp. Biochem. Physiol. 131B:325-337(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- MASS SPECTROMETRY: MW=1381.4; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
 family.
 DR GO; GO:0007218; P. neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.

FT MOD RES 12 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1383 MW; 31209192BFA9D777 CRC64;

Query Match 37.3%; Score 19; DB 1; Length 12;
 Best Local Similarity 42.9%; Pred. No. 9.7e+02;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 GYKNSKF 9
 ||:
 1 GYKPPPF 7

RESULT 8
 CXL4 CONNR STANDARD; PRT; 11 AA.
 ID CXL4 CONNR
 AC P58807;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda-conotoxin Chirya.
 OS Conus marmoreus (Marble cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_Taxid=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20564325; PubMed=10988292;
 RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
 RA Seow K.T., Bay B.-H.;
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide
 pattern and protein folding. Isolation and characterization from the
 venom of Conus marmoreus.";
 RL J. Biol. Chem. 275:39516-39522(2000).
 CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=1237.93; MW ERR=0.21; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.

Query Match 35.3%; Score 18; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYK 5
 ||:
 4 GYK 6

RESULT 9
 CXL4 CONNR STANDARD; PRT; 13 AA.
 ID CXL4 CONNR
 AC P58810;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lambda/chl-conotoxin WtIB (Chi-WtIB).
 OS Conus marmoreus (Marble cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hyposogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_Taxid=42752;
 RN [1]
 RP SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.
 RC TISSUE=Venom;
 RX MEDLINE=21419681; PubMed=11528421;
 RA Sharpe I.A., Gehrmann J., Loughnan M.L., Thomas L., Adams D.A.,

RA Atkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F.,
 Lewis R.J.,
 RT "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
 noradrenaline transporter."
 RL Nat. Neurosci. 4:902-907(2001).
 CC -1- FUNCTION: Inhibits the neuronal noradrenaline transporter.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- PTM: Exists in two forms, due to cis-trans isomerization at His-
 11-Hyp12.
 CC -1- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.
 CC -1- SIMILARITY: Belongs to the chi/lambda-conotoxin family.
 DR PDB: 1IE0; 03-Apr-02.
 KW Neurotoxin; Toxin; Hydroxylation; 3D-structure.
 FT DISULFID 4 13
 FT MOD RES 12 12
 FT SEQUENCE 13 AA; 1382 MW; 277AAC376EAD2B58 CRC64;

Query Match 35.3%; Score 18; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYK 5
 DB 6 GYK 8

RESULT 10
 FARP CALSI STANDARD; PRT; 9 AA.
 ID FARP CALSI
 AC P38495;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRamide-like neuropeptide.
 OS Callinectes sapidus (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunidae; Portunidae; Callinectes.
 OX NCBI_TaxID=6763;
 RN (1)
 RP MEDLINE=92270479; PubMed=1815216;
 RX MEDLINE=92270479; PubMed=1815216;

RA Kravinsk K.G.;
 RT "The identification and structure-activity relations of a
 cardioactive FMRamide-related peptide from the blue crab Callinectes
 sapidus."
 RL Peptides 12:1295-1302(1991).
 CC -1- FUNCTION: Cardioactive peptide.
 CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
 family.
 CC Neuropeptide; Amidation.
 KW MOD RES 9 9
 KW SEQUENCE 9 AA; 1159 MW; 134F0729D5A4045B CRC64;
 SO QUERY Match 33.3%; Score 17; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GYKNS 7
 DB 1 GYKNS 5

RESULT 11
 NXSX_PSETE STANDARD; PRT; 11 AA.
 ID NXSX_PSETE
 AC P59072;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Short neurotoxin NI (Alpha neurotoxin) (Fragment).

OS Pseudonaja textilis (Eastern brown snake).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Elapidae; Acanthophinae; Pseudonaja.
 OX NCBI_TaxID=8673;
 RN (1)
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=9449602; PubMed=10518793;
 RA Gong N.L., Armugam A., Jayaseelan K.;
 RT "Postsynaptic short-chain neurotoxins from Pseudonaja textilis: cDNA
 cloning, expression and protein characterization."
 RL Eur. J. Biochem. 265:982-989(1999).
 CC -1- FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
 acetylcholine receptors (nAChR).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC -1- MASS SPECTROMETRY: MW=6236; METHOD=Electrospray.
 CC -1- MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
 CC -1- SIMILARITY: Belongs to the snake toxin family.
 DR InterPro: IPR003571; Snake toxin.
 DR PROSITE: PS00272; SNAKE_TOXIN; PARTIAL.
 KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
 KW Acetylcholine receptor inhibitor; Multigene family.
 FT UNSURE 3 3
 FT NON TER 11 11
 FT SEQUENCE 11 AA; 1319 MW; 0D1BF0C81B58732B CRC64;

Query Match 33.3%; Score 17; DB 1; Length 11;
 Best Local Similarity 40.0%; Pred. No. 2.1e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKNS 7
 DB 6 GYKNS 10

RESULT 12
 TAI0 TREME STANDARD; PRT; 12 AA.
 ID TAI0 TREME
 AC P01371;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tremorgen A-10.
 OS Tremella mesenterica (Jelly fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
 OC Tremellales; Tremellales; Tremellaceae; Tremella.
 OX NCBI_TaxID=5217;
 RN (1)
 RP SEQUENCE.
 RA Sakagami Y., Yoshida M., Isegai A., Suzuki A.;
 RT "Peptide sex hormones inducing conjugation tube formation in
 RT compatible mating-type cells of Tremella mesenterica."
 RL Science 212:1525-1527(1981).
 CC -1- FUNCTION: Tremorgen A-10 is produced by the a mating-type cells
 and induces formation of conjugation tubes in a mating-type cells.
 CC PIR: A01642; UT060.
 DR Lipoprotein; Prenylation; Methylation; Pheromone.
 KW Lipid 12 12
 KW MOD RES 12 12
 KW SEQUENCE 12 AA; 1246 MW; 84BF574959676DC5 CRC64;

Query Match 31.4%; Score 16; DB 1; Length 12;
 Best Local Similarity 75.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFGY 4
 DB 8 GNGY 11

RESULT 13

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RS19_CLOPP
ID RS19_CLOPP STANDARD; PRT; 14 AA.
AC Q46228;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19
OS Clover proliferation phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phycoplasmata.
OX NCBI_TaxID=35776;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8971198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254 (1994).
CC -!- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (by similarity).
CC -!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; L27011; AAA83938.1; -.
DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KM Ribosomal protein; rRNA-binding.
FT NON_TER
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match 31.4%; Score 16; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 XNSK 8
DB 10 KNOX 13

RESULT 14
ID RS19_LOMBP STANDARD; PRT; 14 AA.
AC Q48878;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19
OS locohah witches'-broom phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Phycoplasmata.
OX NCBI_TaxID=35773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94350802; PubMed=8971198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmas): a basis for
RT their classification.";
RL J. Bacteriol. 176:5244-5254 (1994).
CC -!- FUNCTION: Protein S19 forms a complex with S13 that binds strongly
CC to the 16S ribosomal RNA (by similarity).
CC -!- SIMILARITY: Belongs to the S19P family of ribosomal proteins.
CC -----
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CC -----
DR EMBL; X74750; CA52769.1; -.
DR PIR; S37141; S37141.
KM Ribosomal protein; Repeat; RNA-binding.
FT NON_TER
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match 29.4%; Score 15; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 YNSK 8
DB 2 FXSAK 6

RESULT 16
ID FAR9_ASCSU STANDARD; PRT; 9 AA.

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CC -----
DR EMBL; L27027; AAA83944.1; -.
DR HAMAP; MF_00531; -.
DR InterPro; IPR002222; Ribosomal_S19.
DR PROSITE; PS00323; RIBOSOMAL_S19; PARTIAL.
KM Ribosomal protein; rRNA-binding.
FT NON_TER
SQ SEQUENCE 14 AA; 1642 MW; 20C478EB9FFFE4A8 CRC64;

Query Match 31.4%; Score 16; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 XNSK 8
DB 10 KNOX 13

RESULT 15
ID RS1_ERWCH STANDARD; PRT; 8 AA.
AC P37985;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S ribosomal protein S1 (Fragment).
GN RPSA.
OS Erwina chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RA Douville A., Toussaint A., Faelen M.;
RL submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: BINDS MENA; THIS FACILITATING RECOGNITION OF THE
CC INITIATION POINT. IT IS NEEDED TO TRANSLATE MENA WITH A SHORT
CC SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
CC -!- SIMILARITY: Belongs to the S1P family of ribosomal proteins.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X74750; CA52769.1; -.
DR PIR; S37141; S37141.
KM Ribosomal protein; Repeat; RNA-binding.
FT NON_TER
SQ SEQUENCE 8 AA; 837 MW; 9E18733DC5B339CD CRC64;

Query Match 29.4%; Score 15; DB 1; Length 8;
Best Local Similarity 40.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 YNSK 8
DB 2 FXSAK 6

RESULT 16
ID FAR9_ASCSU STANDARD; PRT; 9 AA.

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AC P43172;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuropeptide AP9.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
 OC Ascarididae; Ascaris.
 OX NCBI_TaxId=6253;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95380362; PubMed=7651904;
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
 RT Ascaris suum";
 RL Peptides 16:491-500(1995).
 CC -I- SIMILARITY: Belongs to the FMRP (FMRamide related peptide)
 CC family.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9
 SQ SEQUENCE 9 AA; 1012 MW; 524F073774176877 CRC64;
 Query Match 29.4%; Score 15; DB 1; Length 9;
 Best Local Similarity 33.3%; Pred. No. 1.4e+05;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 1 GFGYNSKF 9
 DB 1 GIGRPRLRF 9

RESULT 17
 TK02_UREUN STANDARD; PRT; 10 AA.
 AC P40752;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Urechis tachykinin II.
 OS Urechis uncinatus.
 OC Eukaryota; Metazoa; Echinura; Xenopususta; Urechidae; Urechis.
 OX NCBI_TaxId=6432;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=ventral nerve cord;
 RX MEDLINE=93236558; PubMed=8476410;
 RA Ikeda T., Minakata H., Nomoto K., Kubota I., Munooka Y.;
 RT "Two novel tachykinin-related neuropeptides in the echinuroid worm,
 RT Urechis uncinatus";
 RL Biochem. Biophys. Res. Commun. 192:1-6(1993).
 CC -I- FUNCTION: Contractile action on the inner circular body-wall
 CC muscle of the animal.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10
 SQ SEQUENCE 10 AA; 984 MW; 3F58DD79C9C67698 CRC64;
 Query Match 29.4%; Score 15; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.6e+03;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFGY 4
 DB 3 GMSGF 6

RESULT 18
 CA42_LITCI STANDARD; PRT; 11 AA.
 ID CA42_LITCI
 AC P82092;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Caerulein 4.2/4.2Y4.
 OS Litorea citropa (Australian blue mountains tree frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
 OC Pelodyadinae; Litorea.
 OX NCBI_TaxId=94770;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RX MEDLINE=20057701; PubMed=10589099;
 RA Mabinz P.A., Bowie J.H., Tyler M.J.;
 RT "Caerulein-like peptides from the skin glands of the Australian blue
 RT mountains tree frog Litorea citropa. Part 1. Sequence determination
 RT using electrospray mass spectrometry";
 RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
 CC -I- FUNCTION: Hypotensive neuropeptide (probable).
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- TISSUE SPECIFICITY: Skin dorsal glands.
 CC -I- PTM: Isoform 4.2Y4 differs from isoform 4.2 in not being
 CC sulfated.
 CC -I- MASS SPECTROMETRY: MW=1404; METHOD=Electrospray.
 CC -I- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: P500259; GASTRIN; FALSE_NEG.
 KW Amphibian defense peptide; Hypotensive agent; Amidation; Sulfation;
 KW Pyroglutamate carboxylic acid.
 FT MOD_RES 1
 FT MOD_RES 4
 FT MOD_RES 11
 FT MOD_RES 11
 SQ SEQUENCE 11 AA; 1344 MW; 10DAB894F5B861BB CRC64;
 Query Match 29.4%; Score 15; DB 1; Length 11;
 Best Local Similarity 50.0%; Pred. No. 5e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 YKNSKF 9
 DB 4 YTGSHF 9

RESULT 19
 TKC2_CALVO STANDARD; PRT; 11 AA.
 ID TKC2_CALVO
 AC P41518;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Callitachykinin II.
 OS Calliphora vomitoria (Blue blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Calliphora.
 OX NCBI_TaxId=27454;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=95075727; PubMed=7984492;
 RA Lundquist C.T., Cloutens F.L., Holman G.M., Nichols R., Nachman R.J.,
 RA Naessel D.R.;
 RT "Callitachykinin I and II, two novel myotropic peptides isolated from
 RT the blowfly, Calliphora vomitoria, that have resemblances to
 RT tachykinins";
 RL Peptides 15:761-768(1994).
 CC -I- FUNCTION: Myoactive peptide.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 CC -I- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11
 SQ SEQUENCE 11 AA; 1103 MW; 1SD7E3F9C9CDD444 CRC64;
 Query Match 29.4%; Score 15; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 5e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;